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FIG. 1

1 AAAATGTATG GATACAACCTT ACGTTTGATG AAAGATTGG GCTTGAAGAC CCAGAAGATG
TTTTACATAC CTATGTTGAA TGCAAACATAC TTTCTAAACC CGAACTTCTG GGTCTTCTAC

61 ACATATGCAA GTATGATTT GTAGAACGTT AGGAACCCAG TGATGAACT ATATTAGGC
TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC ACTACCTGAA TATAATCCCG

121 GCTGGTGTGG TTCTGGTACT GTACCCAGGAA AACAGATTTC TAAAGGAAAT CAAATTAGGA
CGACCACACC AAGACCATGAA CATGGTCCTT TTGTCCTAAAG ATTCCTTTA GTTTAATCCT

+1 MetAsn IlePheLeu LeuAsnLeuLeu ThrGluGlu ValArgLeu

181 TAAGATTGT ATCTGATGAA TATTTTCCTT CTGAACCTTC TAACAGAGGA GGTAAGATTA
ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGAAAG ATTGTCTCCT CCATTCTAAAT

+1 TyrSerCysThr ProArgAsn PheSerVal SerIleArgGlu GluLeuLys ArgThrAsp

241 TACAGCTGCA CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT
ATGTCGACGT GTGGAGCATT GAAGAGTCAC AGGTATTCCC TTCTGATTT CTCTTGGCTA

+1 ThrIlePheTrp ProGlyCys LeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys

301 ACCATTTCTT GCCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAACTG TGCCTGTTGT
TGGTAAAAGA CCGGTCCAAC AGAGGACCAA TTTGCGACAC CACCCCTGAC ACGGACAACA

+1 LeuHisAsnCys AsnGluCys GlnCysVal ProSerLysVal ThrLysLys TyrHisGlu

361 CTCACAAATT GCAATGAATG TCAATGTGTC CCAAGCAAAG TTACTAAAAA ATACCACGAG
GAGGTGTTAA CGTTACTTAC AGTTACACAG GGTCGTTTC AATGATTTTT TATGGTGCTC

+1 ValLeuGlnLeu ArgProLys ThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal

421 GTCCTTCAGT TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAAATCACT CACCGACGTG
CAGGAAGTCA ACTCTGGTTT CTGGCCACAG TCCCCTAACG TGTTAGTGA GTGGCTGCAC

+1 AlaLeuGluHis HisGluGlu CysAspCys ValCysArgGly SerThrGly Gly
----->
481 GCCCTGGAGC ACCATGAGGA GTGTGACTGT GTGTGCGAGAG GGAGCACAGG AGGATAGCCG
CGGGACCTCG TGGTACTCCT CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC

541 CATCACCAACC ACCAGCTCTT GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA
GTAGTGGTGG TCGTCGAGAA CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT

601 ACGTATGCGT TATCTCCATC CTTAATCTCA GTTGTGGT TCAAGGACCT TTCATCTTC
TGCATACGCA ATAGAGGTAG GAATTAGAGT CAACAAACGA AGTTCTGGAA AAGTAGAAGT

661 GGATTTACAG TGCNTTCTGA AAGAGGAGAC ATCAACAGA ATTAGGAGTT GTGCAACAGC
CCTAAATGTC ACGTAAGACT TTCTCCTCTG TAGTTGTCT TAATCCTCAA CACGTTGTGCG

721 TCTTTGAGA GGAGGCCTAA AGGACAGGGAG AAAAGGTCTT CAATCGTGGAA AAGAAAATTA
AGAAAATCT CCTCCGGATT TCCTGTCCTC TTTTCCAGAA GTTACGACCT TTCTTTAAAT

781 AATGTTGTAT TAAATAGATC ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG
TTACAACATA ATTTATCTAG TGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC

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FIG. 1 (CONTINUED).

841 CTGGGTTCTG TATTCAGTT CTTTCGATAAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA
 GACCCAAGAC ATAAAAGTCAA GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCTTTTT

 901 ACTGTGCAAG TGAGCACCTG ATTCCGTTGC CTTGCTTAAC TCTAAAGCTC CATGTCCTGG
 TGACACGTTC ACTCGTGGAC TAAGGCAACG GAACGAATTG AGATTCGAG GTACAGGACC

 961 GCCTAAAATC GTATAAAATC TGGATTTTTT TTTTTTTTT TGCTCATATT CACATATGTA
 CGGATTTAG CATATTTAG ACCTAAAAAA AAAAAGAAAAA ACGAGTATAA GTGTATACAT

 1021 AACCAAGACA TTCTATGTAC TACAAACCTG GTTTTTAAAA AGGAACATATG TTGCTATGAA
 TTGGTCTTGT AAGATACATG ATGTTGGAC CAAAAATTTC TCCTTGATAC AACGATACTT

 1081 TTAAACTTGT GTCGTGCTGA TAGGACAGAC TGGATTTTC ATATTCCTTA TTAAAATTTC
 AATTTGAACA CAGCACGACT ATCCTGTCTG ACCTAAAAAG TATAAGAAT AATTTAAAG

 1141 TGCCATTTAG AAGAAGAGAA CTACATTCAAT GGTTTGGAAAG AGATAAACCT GAAAAGAAGA
 ACGGTAAATC TTCTTCTCTT GATGTAAGTA CCAAACCTTC TCTATTGGA CTTTCTTCT

 1201 GTGGCCTTAT CTTCACTTTA TCGATAAGTC AGTTTATTTG TTTCATTGTG TACATTTTA
 CACCGGAATA GAAGTGAAT AGCTATTCAAG TCAAATAAAC AAAGTAACAC ATGTTAAAT

 1261 TATTCTCCTT TTGACATTAT AACTGTTGGC TTTTCTAATC TTGTTAAATA TATCTATT
 ATAAGAGGAA AACTGTAATA TTGACAACCG AAAAGATTAG ACAATTAT ATAGATAAAA

 1321 TACCAAAGGT ATTTAATATT CTTTTTTATG ACAACTTAGA TCAACTATTT TTAGCTTGGT
 ATGGTTCCA TAAATTATAA GAAAAAAATAC TGTTGAATCT AGTTGATAAA AATCGAACCA

 1381 AAATTTTCT AAACACAATT GTTATAGCCA GAGGAACAAA GATGATATAA AATATTGTTG
 TTTAAAAAGA TTTGTGTTAA CAATATCGGT CTCCTGTTT CTACTATATT TTATAACAAAC

 1441 CTCTGACAAA AATACATGTA TTTCATTCTC GTATGGTGC AGAGTTAGAT TAATCTGCAT
 GAGACTGTTT TTATGTACAT AAAGTAAGAG CATAACACGA TCTCAATCTA ATTAGACGTA

 1501 TTTAAAAAAC TGAATTGGAA TAGAATTGGT AAGTTGCAA GACTTTTGAA AAATAATTAA
 AAATTTTTG ACTTAACCTT ATCTTAACCA TTCAACGTTT CTGAAAAACT TTTATTAATT

 1561 ATTATCATAT CTTCCATTCC TGTTATTGGA GATGAAAATA AAAAGCAACT TATGAAAGTA
 TAATAGTATA GAAGGTAAGG ACAATAACCT CTACTTTAT TTTCTGTTGA ATACTTCAT

 1621 GACATTCAAGA TCCAGGCCATT ACTAACCTAT TCCCTTTTG GGGAAATCTG AGCCTAGCTC
 CTGTAAGTCT AGGTCGGTAA TGATTGGATA AGGAAAAAAC CCCTTTAGAC TCGGATCGAG

 1681 AGAAAAAACAT AAAGCACCTT GAAAAAGACT TGGCAGCTTC CTGATAAAAGC GTGCTGTGCT
 TCTTTTGTA TTTCGTGGAA CTTTTCTGA ACCGTCGAAG GACTATTCG CACGACACGA

 1741 GTGCAGTAGG AACACATCCT ATTTATTGTG ATGTTGGGT TTTATTATCT TAAACTCTGT
 CACGTCACTT TTGTGTAGGA TAAATAACAC TACAACACCA AAATAATAGA ATTTGAGACA

 1801 TCCATACACT TGTATAAAATA CATGGATATT TTTATGTACA GAAGTATGTC TCTTAACCAAG
 AGGTATGTGA ACATATTAT GTACCTATAA AAATAACATGT CTTCATACAG AGAATTGGTC

 1861 TTCACCTTATT GTACCTGG
 AAGTGAATAA CATGGACC

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FIG. 2. Predicted VEGF-like protein encoded by Incyte contig of 8/12/98

1 MNIFLLNLLT EEVRLYSCTP RNFSVSIREE LKRTDTIFWP GCLLVKRCGG
51 NCACCLHNCN ECQCVP SKVT KKYHEVLQLR PKTGVRGLHK SLTDVALEHH
101 EECDCVCVRGS TGG

FIG. 3. PCR primers for cloning VEGF-X

vegfX1	AAAATGTATGGATAACAAC TTAC
vegfX2	GTTTGATGAAAGATTGGGCTTG
vegfX3	TTTCTAAAGGAAATCAAATTAG
vegfX4	GATAAGATTGTATCTGATG
vegfX5	GATGTCTCCTCTTCAG
vegfX6	GCACAACTCCTAATTCTG
vegfX7	AGCACCTGATTCCGTTGC
vegfX8	TAGTACATAGAATGTTCTGG
vegfX9	AAGAGACATACTTCTGTAC
vegfX10	CCAGGTACAATAAGTGAAGT

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FIG. 4.

JRF) Variants Isolated by PCR (at 8/2/99, all cloned and sequenced at

4154

FIG. 4.

PCR primers- → →

c d

e f

Incyte contig [REDACTED] (8/12/98)

clone 22, 29, 41

clone 52, 59

clone 15, 20

clones 57, 25,
26, 27

2.1kb clones 1,
2, 3

primers- a- vegfX1
(see fig 3) d- vegfX6

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FIG. 5. VEGF-X 5' RACE primers

vegfX11	CCTTAGAAATCTGTTTCTGGTACAG
vegfX12	GGAAAATATTCATCAGATAACAAATCTTATCC
vegfX13	GGTCCAGTGGCAAAGCTGAAGG
vegfX14	CTGGTTCAAGATATCGAATAAGGTCTTCC

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FIG. 6. DNA sequence assembled from in-house clones and 5'RACE

1 TGCCAGAGCA GGTGGGCGCT TCCACCCCAG TGCAGCCTTC CCCTGGCGGT GGTGAAAGAG
ACGGTCTCGT CCACCCCGA AGGTGGGTC ACGTGGAAAG GGGACCGCCA CCACTTTCTC

61 ACTCGGGAGT CGCTGCTTCC AAAGTGCCCCG CGGTGAGTGA GCTCTCACCC CAGTCAGCCA
TGAGCCCTCA GCGACGAAGG TTTCACGGGC GGCACTCACT CGAGAGTGGG GTCAGTCGGT

+2 MetSerLeu PheGlyLeuLeu LeuLeuThr SerAlaLeu AlaGlyGlnArg GlnGlyTh
}-----

121 AATGAGCCTC TTGGGCTTC TCCTGCTGAC ATCTGCCCTG GCCGGCCAGA GACAGGGGAC
TTACTCGGAG AAGCCCGAAG AGGACGACTG TAGACGGGAC CGGCCGGTCT CTGTCCCCCTG

+2 rGlnAlaGlu SerAsnLeuSer SerLysPhe GlnPheSer SerAsnLysGlu GlnAsnG1

181 TCAGGCGGAA TCCAACCTGA GTAGTAAATT CCAGTTTCC AGCAACAAGG AACAGAACGG
AGTCCGCCTT AGGTTGGACT CATCATTTAA GGTCAAAGG TCGTTGTTCC TTGTCTTGCC

+2 yValGlnAsp ProGlnHisGlu ArgIleIle ThrValSer ThrAsnGlySer IleHisSe

241 AGTACAAGAT CCTCAGCATG AGAGAATTAT TACTGTGCT ACTAATGGAA GTATTACAG
TCATGTTCTA GGAGTCGTAC TCTCTTAATA ATGACACAGA TGATTACCTT CATAAGTGTC

+2 rProArgPhe ProHisThrTyr ProArgAsn ThrValLeu ValTrpArgLeu ValAlaVa

301 CCCAAGGTTT CCTCATACTT ATCCAAGAAA TACGGTCTTG GTATGGAGAT TAGTAGCAGT
GGGTTCCAAA GGAGTATGAA TAGGTTCTT ATGCCAGAAC CATACTCTA ATCATCGTCA

+2 lGluGluAsn ValTrpIleGln LeuThrPhe AspGluArg PheGlyLeuGlu AspProGl

361 AGAGGAAAAT GTATGGATAC AACTTACGTT TGATGAAAGA TTTGGGCTTG AAGACCCAGA
TCTCCTTTA CATACTATG TTGAATGCAA ACTACTTCTT AAACCCGAAC TTCTGGGTCT

+2 uAspAspIle CysLysTyrAsp PheValGlu ValGluGlu ProSerAspGly ThrIleLe

421 AGATGACATA TGCAAGTATG ATTTGTAGA AGTTGAGGAA CCCAGTGATG GAACTATATT
TCTACTGTAT ACGTTCATAC TAAAACATCT TCAACTCCTT GGGTCACTAC CTTGATATAA

+2 uGlyArgTrp CysGlySerGly ThrValPro GlyLysGin IleSerLysGly AsnGlnIle

481 AGGGCGCTGG TGTGGTTCTG GTACTGTACC AGGAAAACAG ATTCTAAAG GAAATCAAAT
TCCCGCGACC ACACCAAGAC CATGACATGG TCCCTTTGTC TAAAGATTTC CTTTAGTTA

+2 eArgIleArg PheValSerAsp GluTyrPhe ProSerGlu ProGlyPheCys IleHisTy

541 TAGGATAAGA TTTGTATCTG ATGAATATTT TCCTTCTGAA CCAGGGTTCT GCATCCACTA
ATCTTATTCT AAACATAGAC TACTTATAAG AGGAAGACTT CGTCCCAAGA CGTAGGTGAT

+2 rAsnIleVal MetProGlnPhe ThrGluAla ValSerPro SerValLeuPro ProSerAl

601 CAAATTGTC ATGCCACAAAT TCACAGAACG TGTGAGTCTCT TCACTGTCTAC CGCCCTTCAGC
GTTGTAACAG TACGGTCTTA AGTGTCTTCA ACACTCAGGA ACTCACGATG GGGGAAGTCG

+2 aLeuProLeu AspLeuLeuAsn AsnAlaIle ThrAlaPhe SerThrLeuGlu AspLeuIle

661 TTTGCCACTG GACCTGCTTA ATAATGCTAT AACTGCCCTT ACTACCTTGG AAGACCTTAT
AACCGTGAC CTGGACGAAT TATTACGATA TTGACGGAAA TCATGGAACC TTCTGGAATA

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FIG. 6 (CONTINUED 1).

+2 eArgTyrLeu GluProGluArg TrpGlnLeu AspLeuGlu AspLeuTyrArg ProThrTr

 721 TCGATATCTT GAACCAGAGA GATGGCAGTT GGACTTAGAA GATCTATATA GGCCAACCTTG
AGCTATAGAA CTTGGTCTCT CTACCGTCAA CCTGAATCTT CTAGATATAT CCGGTTGAAC

+2 pGlnLeuLeu GlyLysAlaPhe ValPheGly ArgLysSer ArgValValAsp LeuAsnLe

 781 GCAACTTCTT GGCAAGGCTT TTGTTTTGG AAGAAAATCC AGAGTGGTGG ATCTGAACT
CGTTGAAGAA CCGTTCGAA AACAAAAACC TTCTTTAGG TCTCACCACC TAGACTTGG

 +2 uLeuThrGlu GluValArgLeu TyrSerCys ThrProArg AsnPheSerVal SerIleAr

 841 TCTAACAGAG GAGGTAAAGAT TATACAGCTG CACACCTCGT AACTTCTCAG TGTCCATAAG
AGATTGTCTC CTCCATTCTA ATATGTCGAC GTGTGGAGCA TTGAAGAGTC ACAGGTATTC

 +2 gGluGluLeu LysArgThrAsp ThrIlePhe TrpProGly CysLeuLeuVal LysArgCy

 901 GGAAGAACTA AAGAGAACCG ATACCATTCTT CTGGCCAGGT TGTCTCCTGG TTAAACGCTG
CCTTCTTGAT TTCTCTTGGC TATGGTAAAA GACCGGTCCA ACAGAGGACC AATTGCGAC

 +2 sGlyGlyAsn CysAlaCysCys LeuHisAsn CysAsnGlu CysGlnCysVal ProSerLy

 961 TGGTGGGAAC TGTGCCTGTT GTCTCCACAA TTGCAATGAA TGTCAATGTG TCCCAAGCAA
ACCACCCCTTG ACACGGACAA CAGAGGTGTT AACGTTACAC AGGGTTCGTT

 +2 sValThrLys LysTyrHisGlu ValLeuGln LeuArgPro LysThrGlyVal ArgGlyLe

 1021 AGTTACTAAA AAATACCACG AGGTCCCTCA GTTGAGACCA AAGACCGGTG TCAGGGGATT
TCAATGATT TTTATGGTGC TCCAGGAAGT CAACTCTGGT TTCTGGCAC AGTCCCCTAA

 +2 uHisLysSer LeuThrAspVal AlaLeuGlu HisHisGlu GluCysAspCys ValCysAr

 1081 GCACAAATCA CTCACCGACG TGGCCCTGGA GCACCATGAG GAGTGTGACT GTGTGTGCAG
CGTGTGTTAGT GAGTGGCTGC ACCGGGACCT CGTGGTACTC CTCACACTGA CACACACGTC

 +2 gGlySerThr GlyGly
----->
 1141 AGGGAGCACA GGAGGATAGC CGCATCACCA CCAGCAGCTC TTGCCAGAG CTGTGCAGTG
TCCCTCGTGT CCTCCTATCG GCGTAGTGGT GGTCGTGAG AACGGGTCTC GACACGTCAC

 1201 CAGTGGCTGA TTCTATTAGA GAACGTATGC GTTATCTCCA TCCTTAATCT CAGTTGTTG
GTCACCGACT AAGATAATCT CTTGCATACG CAATAGAGGT AGGAATTAGA GTCAACAAAC

 1261 CTTCAAGGAC CTTTCATCTT CAGGATTAC AGTCATTCT GAAAGAGGAG ACATCAAACA
GAAGTTCCCTG GAAAGTAGAA GTCCTAAATG TCACGTAAGA CTTTCTCCTC TGTAGTTGT

 1321 GAATTAGGAG TTGTGCAACA GCTCTTTGA GAGGAGGCCT AAAGGACAGG AGAAAAGGTC
CTTAATCCTC AACACGTTGT CGAGAAAAGT CTCCTCCGCA TTTCTGTCC TCTTTCCAG

 1381 TTCAATCGTG GAAAGAAAAT TAAATGTTGT ATTAAATAGA TCACCACTA GTTTCAGAGT
AAGTTAGCAC CTTTCTTTA ATTTACAACA TAATTTATCT AGTGGTCGAT CAAAGTCTCA

 1441 TACCATGTAC GTATTCCACT AGCTGGTTC TGTATTCAG TTCTTCGAT ACGGCTTAGG
ATGGTACATG CATAAGGTGA TCGACCCAAG ACATAAAGTC AAGAAAGCTA TGCCGAATCC

 1501 GTAATGTCAG TACAGGAAAA AAACTGTGCA AGTGACCAAG TGATTCGCTT GCCTTGCTTA
CATTACAGTC ATGTCCTTT TTTGACACGT TCACTCGTGG ACTAAGGCAA CGGAACGAAT

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FIG. 6 (CONTINUED 2).

1561 ACTCTAAAGC TCCATGTCTT GGGCTAAAA TCGTATAAAA TCTGGATT TT TTTTTTTTT
TGAGATTCG AGGTACAGGA CCCGGATTT AGCATATTT AGACCTAAAA AAAAAAAA

1621 TTTGCTCATA TTCACATATG TAAACCAGAA CATTCTATGT ACTACAAACC TGGTTTTAA
AAACGAGTAT AAGTGTATAC ATTTGGTCTT GTAAGATACA TGATGTTGG ACCAAAAATT

1681 AAAGGAACTA TGTTGCTATG AATTAAACTT GTGTCGTGCT GATAGGACAG ACTGGATT
TTTCCTTGAT ACAACGATAC TTAATTGAA CACAGCACGA CTATCCTGTC TGACCTAAAA

1741 TCATATTTCT TATTAAAATT TCTGCCATT AGAAGAACAG AACTACATTC ATGGTTGG
AGTATAAAGA ATAATTTAA AGACGGTAA TCTTCTTCTC TTGATGTAAG TACCAAACCT

1801 AGAGATAAAC CTGAAAAGAA GAGTGGCCTT ATCTTCACTT TATCGATAAG CCAGTTTATT
TCTCTATTG GACTTTCTT CTCACCGGAA TAGAAGTGAA ATAGCTATTG GGTCAAATAA

1861 TGTTTCATTG TGTACATTT TATATTCTCC TTTTGACATT ATAACGTGG GCTTTCTAA
ACAAAGTAAC ACATGTAAA ATATAAGAGG AAAACTGTAA TATTGACAAC CGAAAAGATT

1921 TCTTGTAAA TATATCTATT TTTACCAAAG GTATTTATAA TTCTTTTTA TGACAACCTA
AGAACAAATT ATATAGATAA AAATGGTTTC CATAAATTAT AAGAAAAAT ACTGTTGAAT

1981 GATCAACTAT TTTTAGCTTG GTAAATTTT CTAAACACAA TTGTTATAGC CAGAGGAACA
CTAGTTGATA AAAATCGAAC CATTAAAAA GATTTGTGTT AACAAATATCG GTCTCCTTGT

2041 AAGATGATAT AAAATATTGT TGCTCTGACA AAAATACATG TATTTCATTC TCGTATGGTG
TTCTACTATA TTTTATAACA ACAGAGACTGT TTTTATGTAC ATAAAGTAAG AGCATAACAC

2101 CTAGAGTTAG ATTAATCTGC ATTTAAAAAA ACTGAATTGG AATAGAATTG GTAAGTTGCA
GATCTCAATC TAATTAGACG TAAAATTTT TGACTTAACC TTATCTTAAC CATTCAACGT

2161 AAGACTTTT GAAAATAATT AAATTATCAT ATCTTCCATT CCTGTTATTG GAGATGAAAA
TTCTGAAAAA CTTTATTAA TTTAATAGTA TAGAAGGTAA GGACAATAAC CTCTACTTTT

2221 TAAAAAGCAA CTTATGAAAG TAGACATTCA GATCCAGCCA TTACTAACCT ATTCCCTTTT
ATTTTTCGTT GAATACTTTC ATCTGTAAGT CTAGGTGGT AATGATTGGA TAAGGAAAAA

2281 TGGGAAATC TGAGCCTAGC TCAGAAAAAC ATAAAGCACC TTGAAAAAGA CTTGGCAGCT
ACCCCTTAG ACTCGGATCG AGTCTTTTG TATTTCGTGG AACCTTTCT GAACCGTCGA

2341 TCCTGATAAA GCGTGCTGTG CTGTGCAGTA GGAACACATC CTATTTATTG TGATGTTGTG
AGGACTATTT CGCACGACAC GACACGTCAT CCTTGTGTAG GATAAATAAC ACTACAAAC

2401 GTTTTATTAT CTTAAACTCT GTTCCATACA CTTGTATAAA TACATGGATA TTTTTATGTA
CAAATAATA GAATTGAGA CAAGGTATGT GAACATATTT ATGTACCTAT AAAAATACAT

2461 CAGAAGTATG TCTCT
CTCTCATAC AGAGA

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FIG. 7.

New Sequence + Incyte ESTs

1 ATTTGTTAA ACCTTGGAA ACTGGTCAG GTCCAGGTT TGCTTGATC CTTTCAAAA
TAAACAAATT TGGAACCTTGACCAAGTC CAGGTCCAAA ACGAAACTAG GAAAAGTTT

61 ACTGGAGACA CAGAAGAGGG CTTCTAGGAA AAAGTTTGG GATGGGATTA TGTGGAAACT
TGACCTCTGT GTCTTCTCCC GAAGATCCTT TTTCAAAACC CTACCCTAAT ACACCTTTGA

121 ACCCTGCGAT TCTCTGCTGC CAGAGCAGGC TCGGCGCTTC CACCCAGTG CAGCCTTCCC
TGGGACGCTA AGAGACGACG GTCTCGTCCG AGCCGCGAAG GTGGGGTCAC GTCGGAAGGG

181 CTGGCGGTGG TGAAAGAGAC TCAGGGAGTCG CTGCTTCAA AGTCCCCGCC GTGAGTGAGC
GACCGCCACC ACTTTCTCTG AGCCCTCAGC GACGAAGGTT TCACGGCGG CACTCACTCG

+2 Met SerLeuPhe GlyLeuLeu LeuLeuThrSer AlaLeuAl
]-----

241 TCTCACCCCCA GTCAGCCAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC
AGAGTGGGGT CAGTCGGTTT ACTCGGAGAA GCCCGAAGAG GACGACTGTA GACGGGACCG

+2 aGlyGlnArg GlnGlyThrGln AlaGluSer AsnLeuSer SerLysPheGln PheSerSe

301 CGGCCAGAGA CAGGGGACTC AGGCAGAATC CAACCTGAGT AGTAAATTCC AGTTTTCCAG
GCCGGTCTCT GTCCCTGAG TCCGCCTTAG GTTGGACTCA TCATTTAAGG TCAAAAGGTC

+2 rAsnLysGlu GlnTyrGlyVal GlnAspPro GlnHisGlu ArgIleIleThr ValSerTh

361 CAACAAGGAA CAGTACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC
GTTGTTCTT GTCATGCCTC ATGTTCTAGG AGTCGTACTC TCTTAATAAT GACACAGATG

+2 rAsnGlySer IleHisSerPro ArgPhePro HisThrTyr ProArgAsnThr ValLeuVa

421 TAATGGAAGT ATTACACAGCC CAAGGTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT
ATTACCTTCA TAAGTGTGG GTTCAAAGG AGTATGAATA GGTTCTTAT GCCAGAACCA

+2 lTrpArgLeu ValAlaValGlu GluAsnVal TrpIleGln LeuThrPheAsp GluArgPh

481 ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT
TACCTCTAAAT CATCGTCATC TCCTTTACA TACCTATGTT GAATGCAAAC TACTTTCTAA

+2 eGlyLeuGlu AspProGluAsp AspIleCys LysTyrAsp PheValGluVal GluGluPr

541 TGGGCTTCAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC
ACCCGAACCTT CTGGGTCTTC TACTGTATAAC GTTCATACTA AAACATCTTC AACTCCTTGG

+2 oSerAspGly ThrIleLeuGly ArgTrpCys GlySerGly ThrValProGly LysGlnIl

601 CAGTGATGGA ACTATATTAG GGCGCTGGTG TGGTTCTGGT ACTGTACCAAG GAAAACAGAT
GTCACTACCT TGATATAATC CCGCGACCAC ACCAAGACCA TGACATGGTC CTTTTGTCTA

+2 eSerLysGly AsnGlnIleArg IleArgPhe ValSerAsp GluTyrPhePro SerGluPr

661 TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC
AAGATTTCT GTAGTTAAT CCTATTCTAA ACATAGACTA CTTATAAAAG GAAGACTTGG

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FIG. 7 (CONTINUED 1).

+2 oGlyPheCys IleHisTyrAsn IleValMet ProGlnPhe ThrGluAlaVal SerProSe

721 AGGGTTCTGC ATCCACTACA ACATTGTCAAT GCCACAAATTC ACAGAAGCTG TGAGTCCTTC
TCCCAAGACG TAGGTGATGT TGAAACAGTA CGGTGTTAAC TGTCTTCGAC ACTCAGGAAG

+2 rValLeuPro ProSerAlaLeu ProLeuAsp LeuLeuAsn AsnAlaIleThr AlaPheSe

781 AGTGCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTAG
TCACGATGGG GGAAGTCGAA ACGGTGACCT GGACGAATTA TTACGATATT GACGGAAATC

+2 rThrLeuGlu AspLeuIleArg TyrLeuGlu ProGluArg TrpGlnLeuAsp LeuGluAs

841 TACCTGGAA GACCTTATTG GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA
ATGGAACCTT CTGGAATAAG CTATAGAACT TGGTCTCTCT ACCGTCAACC TGAATCTTCT

+2 pLeuTyrArg ProThrTrpGln LeuLeuGly LysAlaPhe ValPheGlyArg LysSerAr

901 TCTATATAGG CCAAACCTGGC AACTTCTTGG CAAGGCTTT GTTTTGAA GAAAATCCAG
AGATATATCC GGTTGAACCG TTGAAGAACCC GTTCCGAAAA CAAAAACCTT CTTTTAGGTC

+2 gValValAsp LeuAsnLeuLeu ThrGluGlu ValArgLeu TyrSerCysThr ProArgAs

961 AGTGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA
TCACCACCTA GACTTGGAAAG ATTGTCTCCT CCATTCTAAT ATGTCGACGT GTGGAGCATT

+2 nPheSerVal SerIleArgGlu GluLeuLys ArgThrAsp ThrIlePheTrp ProGlyCy

1021 CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTCTT GGCCAGGTTG
GAAGAGTCAC AGGTATTCCC TTCTTGATT CTCTTGGCTA TGGTAAAAGA CCGGTCCAAC

+2 sLeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys LeuHisAsnCys AsnGluCy

1081 TCTCCTGGTT AAACGCTGTG GTGGGAACGT TGCGCTGTGT CTCCACAATT GCAATGAATG
AGAGGACCAA TTTGCGACAC CACCCCTGAC ACGGACAACA GAGGTGTTAA CGTTACTTAC

+2 sGlnCysVal ProSerLysVal ThrLysLys TyrHisGlu ValLeuGlnLeu ArgProLy

1141 TCAATGTGTC CCAAGCAAAG TTACTAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA
AGTTACACAG GGTCGTTTC AATGATTTTT TATGGTGCTC CAGGAAGTCA ACTCTGGTTT

+2 sThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal AlaLeuGluHis HisGluGl

1201 GACCGGTGTC AGGGGATTGC ACAAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA
CTGGCCACAG TCCCCTAACG TGTGTTAGTGA GTGGCTGCCAC CGGGACCTCG TGGTACTCCT

+2 uCysAspCys ValCysArgGly SerThrGly Gly

----->

1261 GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG CATCACCAACC AGCAGCTCTT
CACACTGACA CACACGTCTC CCTCGTGTCC TCCTATCGGC GTAGTGGTGG TCGTCGAGAA

1321 GCCCAGAGCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA ACGTATGCGT TATCTCCATC
CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT TGCATACGCA ATAGAGGTAG

1381 CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTCA GGATTTACAG TGCATTCTGA
GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT CCTAAATGTC ACGTAAGACT

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FIG. 7 (CONTINUED 2)

1441 AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC TCTTTGAGA GGAGGCCTAA
 TTCTCCTCTG TAGTTGTCT TAATCCTCAA CACGTTGTCG AGAAAATCT CCTCCGGATT

 1501 AGGACAGGAG AAAAGGTCTT CAATCGTGG AAGAAAATTA AATGTTGTAT TAAATAGATC
 TCCTGTCCTC TTTTCCAGAA GTTAGCACCT TTCTTTAAT TTACAACATA ATTTATCTAG

 1561 ACCAGCTAGT TTCAGAGTTA CCATGTACGT ATTCCACTAG CTGGGTTCTG TATTCAGTT
 TGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC GACCCAAGAC ATAAAGTCAA

 1621 CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA ACTGTGCAAG TGAGCACCTG
 GAAAGCTATG CCGAATCCC TTACAGTCAT GTCCTTTTG TGACACGTT ACCTCGTGGAC

 1681 ATTCCGTTGC CTTGGCTTAA CTCTAAAGCT CCATGTCTG GGCTAAAAT CGTATAAAAAT
 TAAGGCAACG GAACCGAATT GAGATTCGA GGTACAGGAC CCGGATTTA GCATATTTA

 1741 CTGGATTTT TTTTTTTTT TTGCGCATAT TCACATATGT AAACCAGAAC ATTCTATGTA
 GACCTAAAAA AAAAAAAA AACGCGTATA AGTGTATACA TTTGGTCTTG TAAGATACAT

 1801 CTACAAACCT GGTTTTAAA AAGGAACTAT GTTGCTATGA ATTAAACTTG TGTCATGCTG
 GATGTTGGA CCAAAATTT TTCCTTGATA CAACGATACT TAATTGAAAC ACAGTACGAC

 1861 ATAGGACAGA CTGGATTTT CATATTCTT ATTAAAATTT CTGCCATTTA GAAGAAGAGA
 TATCCTGTCT GACCTAAAAA GTATAAGAA TAATTAAA GACGGTAAAT CTTCTCTCT

 1921 ACTACATTCA TGGTTGGAA GAGATAAACC TGAAAAGAAG AGTGGCTTA TCTTCACCTT
 TGATGTAAGT ACCAAACCTT CTCTATTGG ACTTTCTTC TCACCGGAAT AGAAGTGAAA

 1981 ATCGATAAGT CAGTTTTTT GTTTCATTGT GTACATTTTT ATATTCTCCT TTTGACATTA
 TAGCTATTCA GTCAAATAAA CAAAGTAACA CATGAAAAA TATAAGAGGA AACTGTAAT

 2041 TAACTGTTGG CTTTTCTAAT CTTGTTAAAT ATATCTATTT TTACCAAAGG TATTTAATAT
 ATTGACAACC GAAAAGATTA GAACAATTAA TATAGATAAA AATGGTTCC ATAAATTATA

 2101 TCTTTTTAT GACAACCTAG ATCAACTATT TTTAGCTTGG TAAATTTTC TAAACACAAT
 AGAAAAATA CTGTTGAATC TAGTTGATAA AAATCGAACC ATTAAAAAG ATTTGTGTTA

 2161 TGTTATGCC AGAGGAACAA AGATGATATA AAATATTGTT GCTCTGACAA AAATACATGT
 ACAATATCGG TCTCCTGTT TCTACTATAT TTTATAACAA CGAGACTGTT TTTATGTACA

 2221 ATTTCAATTCT CGTATGGTGC TAGAGTTAGA TTAATCTGCA TTTAAAAAAA CTGAATTGGA
 TAAAGTAAGA GCATACCAAG ATCTCAATCT AATTAGACGT AAAATTTTT GACTTAACCT

 2281 ATAGAATTGG TAAGTTGCAG AGACTTTTG AAAATAATTA AATTATCATA TCTTCACATTC
 TATCTTAACC ATTCAACGTT TCTGAAAAAC TTTTATTAAT TTAATAGTAT AGAAGGTAAG

 2341 CTGTTATTGG AGATGAAAAT AAAAGCAAC TTATGAAAGT AGACATTCAAG ATCCAGCCAT
 GACAATAACC TCTACTTTA TTTTCGTTG AATACTTCA TCTGTAAGTC TAGGTCGGTA

 2401 TACTAACCTA TTCTTTTTT GGGAAATCT GAGCCTAGCT CAGAAAAACA TAAAGCACCT
 ATGATTGGAT AAGGAAAAAA CCCCTTTAGA CTCGGATCGA GTCTTTTGT ATTCGTTGGA

 2461 TGAAAAAGAC TTGGCAGCTT CCTGATAAAG CGTGCTGTGC TGTGCACTAG GAACACATCC
 ACTTTTCTG AACCGTCGAA GGACTATTTC GCACGACACG ACACGTCATC CTTGTGTTAGG

 2521 TATTTATTGT GATGTTGTGG TTTTATTATC TTAAACTCTG TTCCATACAC TTGTATAAAAT
 ATAATAACA CTACAACACC AAAATAATAG AATTGAGAC AAGGTATGTG AACATATTTA

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FIG. 7 (CONTINUED 3).

2581 ACATGGATAT TTTTATGTAC AGAAGTATGT CTCTTAACCA GTTCACTTAT TGTACTCTGG
TGTACCTATA AAAATACATG TCTTCATACA GAGAATTGGT CAAGTGAATA ACATGAGACC

2641 CAATTAAAAA GAAAATCAGT AAAATATTTT GCTTGTAAGA TGCTTAATAT CGTGCCTAGG
GTTAAATTTC CTTTAGTCA TTTTATAAAA CGAACATTAA ACGAATTATA GCACGGATCC

2701 TTATGTGGTG ACTATTTGAA TCAAAAATGT ATTGAATCAT CAAATAAAAG AATGTGGCTA
AATACACCAC TGATAAAACTT AGTTTTACA TAACTTAGTA GTTTATTTTC TTACACCGAT

2761 TTTTGGGGAG AAAATT
AAAACCCCTC TTTTAA

FIG. 8. Additional oligonucleotides used for amplification of entire coding region

5'-1	TTTGTAAACCTGGAACTGG
5'-2	GTCCAGGTTTGCTTGATCC

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FIG. 9. DNA Sequence Of Clones 4 & 7, Identical Clones Containing The Entire Open Reading Frame

1 TTTGTTAAA CCTTGGAAA CTGGTCAGG TCCAGGTTT GCTTGATCC TTTCAAAAA
AAACAAATTG GGAACCCTT GACCAAGTCC AGGTCAAAA CGAAACTAGG AAAAGTTTT

61 CTGGAGACAC AGAAGAGGGC TCTAGGAAA AGTTTGAT GGGATTATGT GGAAACTACC
GACCTCTGTG TCTTCTCCCG AGATCCTTT TCAAAACCTA CCCTAATACA CCTTGATGG

121 CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG CCTTCCCCCTG
GACGCTAAGA GACGACGGTC TCGTCCGAGC CGCGAAGGTG GGGTCACGTC GGAAGGGAC

181 GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCCCGGTG AGTGAGCTCT
CGCCACCACT TTCTCTGAGC CCTCAGCGAC GAAGGTTCA CGGGCGGCAC TCACTCGAGA

+2 MetSer LeuPheGly LeuLeuLeu LeuThrSerAla LeuAlaG1
]-

241 CACCCCAGTC AGCCAAATGA GCCTCTCGG GCTTCTCCTG CTGACATCTG CCCTGGCCGG
GTGGGGTCAG TCGGTTTACT CGGAGAACCC CGAAGAGGAC GACTGTAGAC GGGACCGGGC

+2 yGlnArgGln GlyThrGlnAla GluSerAsn LeuSerSer LysPheGlnPhe SerSerAs

301 CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT TTTCCAGCAA
GGTCTCTGTC CCCTGAGTCC GCCTTAGGTT GGACTCATCA TTTAAGGTCA AAAGGTCGTT

+2 nLysGluGln AsnGlyValGln AspProGln HisGluArg IleIleThrVal SerThrAs

361 CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG TGTCTACTAA
GTTCCCTTGTC TTGCCTCATG TTCTAGGAGT CGTACTCTCT TAATAATGAC ACAGATGATT

+2 nGlySerIle HisSerProArg PheProHis ThrTyrPro ArgAsnThrVal LeuValTr

421 TGGAAGTATT CACAGCCAA GGTTCTCTCA TACTTATCCA AGAAATACGG TCTTGGTATG
ACCTTCATAA GTGTCGGGTT CCAAAGGAGT ATGAATAGGT TCTTTATGCC AGAACCATAC

+2 pArgLeuVal AlaValGluGlu AsnValTrp IleGlnLeu ThrPheAspGlu ArgPheG1

481 GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACCTT ACCTTGATG AAAGATTTGG
CTCTAACATCGT CATGTTGAA TGCAAACATAC TTTCTAACCC ACC

+2 yLeuGluAsp ProGluAspAsp IleCysLys TyrAspPhe ValGluValGlu GluProSe

541 GCTTGAAAGAC CCAGAAAGATG ACATATGCCA GTATGATTT GTAGAAGTTG AGGAACCCAG
CGAACTTCTG GGTCTCTAC TGTATACGTT CATACTAAA CATCTCAAC TCCTGGGTC

+2 rAspGlyThr IleLeuGlyArg TrpCysGly SerGlyThr ValProGlyLys GlnIleSe

601 TGATGGAACT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC
ACTACCTTGA TATAATCCCG CGACCAACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG

+2 rLysGlyAsn GlnIleArgIle ArgPheVal SerAspGlu TyrPheProSer GluProG1

661 TAAAGGAAAT CAAATTAGGA TAAGATTTGT ATCTGATGAA TATTTCTT CTGAACCAGG
ATTTCTTTA GTTTAACCT ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTCGGTCC

FIG. 9 (CONTINUED). 14/54

+2 yPheCysIle HisTyrAsnIle ValMetPro GlnPheThr GluAlaValSer ProSerVa

721 GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTACACA GAAGCTGTGA GTCCTTCAGT
CAAGACGTAG GTGATGTTGT AACAGTACGG TGTAAAGTGT CTTCGACACT CAGGAAGTCA

+2 lLeuProPro SerAlaLeuPro LeuAspLeu LeuAsnAsn AlaIleThrAla PheSerTh

781 GCTACCCCCCT TCAGCTTGC CACTGGACCT GCTTAATAAT GCTATAACTG CCTTTAGTAC
CGATGGGGGA AGTCGAAACG GTGACCTGGA CGAATTATTA CGATATTGAC GGAAATCATG

+2 rLeuGluAsp LeuIleArgTyr LeuGluPro GluArgTrp GlnLeuAspLeu GluAspLe

841 CTTGGAAGAC CTTATTGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT TAGAAGATCT
GAACCTTCTG GAATAAGCTA TAGAACCTGG TCTCTCTACC GTCAACCTGA ATCTTCTAGA

+2 uTyrArgPro ThrTrpGlnLeu LeuGlyLys AlaPheVal PheGlyArgLys SerArgVa

901 ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTGTT TTTGGAAGAA AATCCAGAGT
TATATCCGGT TGAACCGTTG AAGAACCGTT CCGAAAACAA AAACCTTCTT TTAGGTCTCA

+2 lValAspLeu AsnLeuLeuThr GluGluVal ArgLeuTyr SerCysThrPro ArgAsnPh

961 GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC CTCGTAACCT
CCACCTAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG TCGACGTGTG GAGCATTGAA

+2 eSerValSer IleArgGluGlu LeuLysArg ThrAspThr IlePheTrpPro GlyCysLe

1021 CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATAACC ATTTTCTGGC CAGGTTGTCT
GAGTCACAGG TATTCCCTTC TTGATTTCTC TTGGCTATGG TAAAAGACCG GTCCAACAGA

+2 uLeuValLys ArgCysGlyGly AsnCysAla CysCysLeu HisAsnCysAsn GluCysG1

1081 CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA ATGAATGTCA
GGACCAATTG GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT TACTTACAGT

+2 nCysValPro SerLysValThr LysLysTyr HisGluVal LeuGlnLeuArg ProLysTh

1141 ATGTGTCCCCA AGCAAAGTTA CTAAAAAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC
TACACAGGGT TCGTTCAAT GATTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTCTG

+2 rGlyValArg GlyLeuHisLys SerLeuThr AspValAla LeuGluHisHis GluGluCy

1201 CGGTGTCAGG GGATTGCAAC AATCACTCAC CGACGTGGCC CTGGAGCACC ATGAGGAGTG
GCCACAGTCC CCTAACGTGT TTAGTGTGAGTG GCTGCACCGG GACCTCGTGG TACTCCTCAC

+2 sAspCysVal CysArgGlySer ThrGlyGly
----->
1261 TGACTGTGTG TGCAAGAGGG A GCACAGGAGG ATAGCCGCAT CACCACCAAGC AGCTCTTGCC
ACTGACACAC ACGTCTCCCT CGTGTCTCC TATCGCGTA GTGGTGGTCG TCGAGAACGG

1321 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT
GTCTCGACAC GTCACGTAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA

1381 AATCTCAGTT GTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG
TTAGAGTCAA CAAACGAAGT TCCTGGAARG TAGAAGTCCCT AAATGTCACG TAAGACTTTC

1441 AGGAGACATC AAACAGAATT AGGAGTTGTG CAA
TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTT

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FIG. 10. Predicted Full-length Polypeptide Sequence

1 MSLFGLLLLT SALAGQRQGT QAESNLSSKF QFSSNKEQYG VQDPQHERII
51 TVSTNGSIHS PRFPHTYPRN TVLVWRLVAV EENVWIQLTF DERFGLEDPE
101 DDICKYDFVE VEEPSDGTIL GRWCGSGTVP GKQISKGNQI RIRFVSDEYF
151 PSEPGFCIHY NIVMPQFTEA VSPSVLPPSA LPLDLLNNAI TAFSTLEDLI
201 RYLEPERWQL DLEDLYRPTW QLLGKAFVFG RKSRVVDLNL LTEEVRLYSC
251 TPRNFSVSIR EELKRTDTIF WPGCLLVKRC GGNACCLHN CNECQCVP SK
301 VTKKYHEVHQ LRPKTGVRGL HKSLTDVALE HHEECDCVCR GSTGG

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FIG. 11

Alignment of VEGF-X with Other VEGFs

VEGF_HUMAN :	*	20	*	40	*	
PLGF_HUMAN :	-	-	-	-	-	:
VEGB_HUMAN :	-	-	-	-	-	:
VEGC_HUMAN :	-	-	-	-	-	:
VEGD_HUMAN :	-	-	-	-	-	:
990126vegx :	MSLFGLLLTSLAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII					50

VEGF_HUMAN :	60	*	80	*	100	
PLGF_HUMAN :	-	-	-	-	-	:
VEGB_HUMAN :	-	-	-	-	-	:
VEGC_HUMAN :	-	-	-	-	-	:
VEGD_HUMAN :	-	-	-	-	-	:
990126vegx :	TVSTNGSIHSPRFPTHYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPE					100

VEGF_HUMAN :	*	120	*	140	*	
PLGF_HUMAN :	-	-	-	-	-	:
VEGB_HUMAN :	-	-	-	-	-	:
VEGC_HUMAN :	-	-	MHLLGFFSVACSLAALLPGPREAPAAAA			30
VEGD_HUMAN :	-	-	-	MYREWWVVNV		10
990126vegx :	DDICKYDFVEV--EEPSDGTTILGRWCSGTVPKGQISKGNQIRIRFVSDE					148

VEGF_HUMAN :	160	*	180	*	200	
PLGF_HUMAN :	-	-	-	-	MN	2
VEGB_HUMAN :	-	-	-	-	MP	2
VEGC_HUMAN :	ALESGLLDSLDAEPDAGEATAYASKDLEEQLRSVSSVDELMVTLYPEYWKM					80
VEGD_HUMAN :	FMMLYVQLVQGSNEHGPVKRSSQSTLERSEQIARAASSLEELLRITHSE					60
990126vegx :	YFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDNNNAITAFSTLED					198

VEGF_HUMAN :	*	220	*	240	*	
PLGF_HUMAN :	FLLSWVHWSLALLYLHHAKWSQAAPMAEGGGQNHHEVVKFMD-VYQR SY					51
VEGB_HUMAN :	VMRLFPCFLQLLAGLPAVPPQQWALSAGNGSSEVEVVPFQE-VWGR SY					51
VEGC_HUMAN :	--MSPLLRRLLLAALLQLAPAQAPVSQPDAPGHQRKVVSVID-VYTRAT					46
VEGD_HUMAN :	YKCQLRKGGWQHNREQANLNSRTEETIKFAAAHYNTEILKSIDNEWRKTQ					130
990126vegx :	DWKWLWRCLRLKSFSTSMDRSASHRSTRFAATFYDIETLKVIDEEWQRTQ					110
	LIRYLEPERWQLDLEDLYRPTWQLLGKAFVGRKSRVVDLNLLTEEVRLY					248

VEGF_HUMAN :	260	*	280	*	300	
PLGF_HUMAN :	CHPIETLVDIFQEPYDIEYIFKPSCVPLMRCCGG--CCND--EGLECV P					96
VEGB_HUMAN :	CRALERLVDVVSYPSEVEHMESPSCVSLLRCTG--CCGD--ENLHCVP					96
VEGC_HUMAN :	CQPREVVVPLTVELMGTVAKQLVPSCVTVQRCCGG--CCPD--DGLECV P					91
VEGD_HUMAN :	CMPREVCIDVGKEFGVATNTFFKPPCFSVYRCCGG--CCNS--EGLOCMN					175
990126vegx :	CSPRETCVEVASIELGKSTNTFFKPPCFSVYRCCGG--CCNE--ESLICMN					155
	SCTPRNFSVSIRIELKRTDTIFWPGLLVLKRCGGNCACCLHNCNECQCV P					298

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FIG. 11 (CONTINUED).

	* 320 *	340	*	
VEGF_HUMAN	: TEESNITM QI M R I K PHQG-----QHIGEMSFLQHNK C E C RPKKDRARQE K			: 141
PLGF_HUMAN	: VETANVTM Q LL K IRSGDR-----PSYVELTFSQHVR C ECRPLRE K M K PER			: 141
VEGB_HUMAN	: TGQHQV R MQ I LM I RYPS-----SQLGEMSLEEH H SQ C ECRPKKKDSAVKP			: 135
VEGC_HUMAN	: TSTS Y LS K T L FETTVPLSQG---PKPVT I S F ANHT T SCRCMSKLDVYRQV H			: 222
VEGD_HUMAN	: TSTS Y ISK Q LF E ISVPLTSV---PELVPVKVANHT G C K L PTAPRH P YS I			: 202
990126vegx	: SKVTKKYHEVLQLRPKTGVRLHKSLTD V A L E H EECD Q VCRGSTGG---			: 345

	360	*	380	*	400	*	
VEGF_HUMAN	: KSVRGKG G QKRKRKKSR Y KWSVP-----						: 166
PLGF_HUMAN	: -----						: -
VEGB_HUMAN	: DS P R-----						: 139
VEGC_HUMAN	: SII R SLPATLPQC Q AANKTCPTNYM W NNHICRCL A QEDFMFSSDAGDD S						: 272
VEGD_HUMAN	: IRRSI Q I P EEDRC S H S KKLC P IDMLWDSNKCK C V L QEENPLAGT-----						: 246
990126vegx	: -----						: -

	*	420	*	440	*	460	*	
VEGF_HUMAN	: -----							: -
PLGF_HUMAN	: -----							: -
VEGB_HUMAN	: -----							: -
VEGC_HUMAN	: TDGFHD I CGPN K ELDEETCQCVCRAGLRPASC G PH K ELDRNSCQC V CKNK							: 322
VEGD_HUMAN	: -----EDHSHL Q EPA L CG P							: 260
990126vegx	: -----							: -

	460	*	480	*	500	*		
VEGF_HUMAN	: -----CGPCSER R KHLFVQDPQTCKC-SCKNTDS R CKARQ L NER						: 206	
PLGF_HUMAN	: -----CGDAVPRR-----						: 149	
VEGB_HUMAN	: -----PLCPRCTQHH Q RPDPRTCR C R C RRRSFLRC Q GRGLELNPD						: 179	
VEGC_HUMAN	: LFPSQC G ANREFDENTCQCVC K RTCPRNQPLNPG K CACECTESP P Q K LL K						: 372	
VEGD_HUMAN	: HMMFD E DRCECV K TPCP K D L I Q HP K N C SC F ECKESLETCC Q K H KLF H PD						: 310	
990126vegx	: -----							: -

	*	520	*	540	*		
VEGF_HUMAN	: TCRC D KP R R-----						: 215
PLGF_HUMAN	: -----						: -
VEGB_HUMAN	: TCRC R KL R R-----						: 188
VEGC_HUMAN	: GKKFHH Q TCS C YRRPCTNRQ K ACE P GF S Y SE E V CRCV P SY W K R P Q M S						: 419
VEGD_HUMAN	: TCS C ED R CP F HTRPCAS G K T ACAK H CRFP K E K RA Q G P HS R K N P-----						: 354
990126vegx	: -----						: -

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FIG. 12.

Variant Polypeptide Sequences

	*	20	*	40	*	
FL_seq	:	MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII			:	50
clone41	:	MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII			:	50
clone20	:	MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERII			:	50
	60	*	80	*	100	
FL_seq	:	TVSTNGSIHSPRFPHTYPRNTVLWWRLVAVEENVWIOLTFDERFGLEDPE			:	100
clone41	:	TVSTNGSIHSPRFPHTYPRNTVLWWRLVAVEENVWIOLTFDERFGLEDPE			:	100
clone20	:	TVSTNGSIHSPRFPHTYPRNTVLWWRLVAVEENVWIOLTFDERFGLEDPE			:	100
	*	120	*	140	*	
FL_seq	:	DDICKYDFVEVEE PSDGT TILGRWC GSGT VPGKQIS KGNQ I RIFR FVSDEYF			:	150
clone41	:	DDICKYDFVEVEE PSDGT TILGRWC GSGT VPGKQIS KGNQ I RIFR FVSDEYF			:	150
clone20	:	DDICKYDFVEVEE PSDGT TILGRWC GSGT VPGKQIS KGNQ I RIFR FVSDEYF			:	150
	160	*	180	*	200	
FL_seq	:	PSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI			:	200
clone41	:	PSEPSNRGGKIIQLHTS-----			:	167
clone20	:	PSEPGFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLI			:	200
	*	220	*	240	*	
FL_seq	:	RYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLYSC			:	250
clone41	:	-----			:	-
clone20	:	RYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNLLTE-----			:	243
	260	*	280	*	300	
FL_seq	:	TPRNFSVSIREELKRTDTIFWP GCLLV KRC GGNCACCL HNCNECQC VPSK			:	300
clone41	:	-----			:	-
clone20	:	-----			:	-
	*	320	*	340	*	
FL_seq	:	VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG			:	345
clone41	:	-----			:	-
clone20	:	-----EV LQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG			:	282

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FIG. 13. Primers for Expression of VEGF-X

E.coli expression of domain-

vegx-6 AATTGGATCCGAGAGTGGTGGATCTGAACC

vegx-7 AATTGGATCCGGGAAGAAAAATCCAGAGTGG

vegx-8 GGTTGAATTCAATTATTTTTAGTAACCTTGCTGGACAC

vegX-9 AATTGAATTCAATTATCCTCCTGTGCTCCCTC

Baculovirus/insect cell expression of full-length protein-

vegbac1

AATTGGATCCGGAGTCTCACCATCACCAACCATCATGAATCCAACCTGAGTAGTAAATTC
C

vegbac2

AATTGAATTCGCTATCCTCCTGTGCTCCCTCTGC

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FIG. 14.

>3993180H1 LUNGNON03 INCYTE
 CACAAATCACTCACCGACGTGGCCCTGGAGCACCAGTGGGNGTGTGACTGTGTGCAGAGGGAGCACAGGAGGATAGCC
 GCATCACCACCAGCAGCTCTGCCAGAGCTGTGCAGTCAGTGGCTATTAGAGAACGTATGCCTTATCTCCAT
 CCTTAATCTCAGTTGTTGCTCAAGGACCTTCATCTCAGGATTACAGTCATCTGAAAGAGGAGACATCAAACAG
 AATTAGGAGTTGTCAACAGCTTTGAGAGGAGGCTAAGGACAGGAGAANAGGTCTT
>3510192H1 CONCNOT01 INCYTE
 TGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCCTTATCTCCATCCTTAATCTCAGTTGTTGCTTCAGGACCTT
 TCATCTTCAGGATTACAGTCATTCTGAAAGAGGAGACATCAAACAGAACATTAGGAGTTGTCAACAGCTTTGAGG
 GAGGCCTAAAGGACAGGAGAAAAGGTCTCAATCGTGGAAAGAAAATTAAATGTTTATTAAATAGATCACCAGCTAGTT
 TCAGAGTTACCATGTACGTATTCCACTAGCTGGGTCTGTATT
>2559870H1 ADRETUT01 INCYTE
 CACGAGGTCCCTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCA
 TGAGGAGTGTGACTGTGTGTCAGAGGGAGCACAGGGGATAGCCGCATCACCACCAGCAGCTTGCAGGACCTTCAGGAC
 AGTCAGTGGCTGATTCTATTAGAGAACGTATGCCTTATCTCCATCCTTAATCTCAGTTGTTGCTTCAGGACCTTCA
 TCTCAGGATTACAGTCATTGAAAGAGGAGA
>3979767H1 LUNGTUT08 INCYTE
 GGAGGATAGCCGCATCACCAACAGCAGCTTGCAGAGCTGTGCACTGCAGTGGCTGATTCTATTAGAGAACGTATGC
 GTTATCTCCATCCTTAATCTCAGTTGTTGCTTCAGGACCTTCATCTCAGGATTACAGTCATTCTGAAAGAGGAG
 ACATCAAACAGAACATTAGGAGTTGTCAACAGCTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTCAATCGT
 GAAAGAANATTAAATGTTTATTAAATAGACACCAGCT
>3980011H1 LUNGTUT08 INCYTE
 GGAGGATAGCCGCATCACCAACAGCAGCTTGCAGGAGCTGTGCACTGCAGTGGCTGATTCTATTAGAGAACGTATGC
 GTTATCTCCATCCTTAATCTCAGTTGTTGCTTCAGGACCTTCATCTCAGGATTACATGCATTCTGAAAGAGGAGA
 CATCAAACAGAACATTAGGAGTTGTCAACAGCTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTCAATCGT
 AAAGAAAATTAAATGTTTATTAAATAGACACCA
>4825396H1 BLADDIT01 INCYTE
 GAGAACCGATACCATTCTGCCAGGGTGTCTCCCTGGTAAACGCTGGTGGGGAACTGTGCCTGTTGCTCCACAATT
 GCAATGAATGTCAATGTGTCCAAGAACAGTTACTAAAAAAATACCACGGGTCTTCAGTTGAGACCAAAAGACCGGTG
 AGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCAGTGGAGTGTGACTGTGTGCAAGAGGAGCACAGG
 AGGATAGCCGCATCACCA
>3073703H1 BONEUNT01 INCYTE
 AGAAAATCCAGAGTGGTGGACTGAACCTTCTAACAGAGGAGGTAAGATATAACAGCTGCACACCTCGTAACCTCTCA
 GTCCATAAGGGAAAGAACCTAAAGAGAACCGATACCAATTCTGCCAGGGTGTCTCCCTGGTAAACGCTGGTGGGGAACT
 GTGCCTGTTGTCCTCCACAATTGCAATGAATGTCAATGTGTCCAAGAACAGTTACTAAAAAAATACCACGAGGTCTTCAG
 TTGAGACCAAAAGACCGGTGTCAGGGGATTGCACAAATCA
>1302516H1 PLACNOT02 INCYTE
 AGAAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCCTCTGAACCTTCTAACAGAGGAGGTAAGGATTATAC
 AGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAAGAACCTAAAGAGAACCGATACCATTTCCTGCCAGGGTGTCT
 CCTGGTTAACGCTGTGGGAACTGTGCCTGTTGTCCTCCACAATTGCAATGAATGTCAATGTGTCCCAGGAAAGTT
 ACTAAAAAAATACCACGAGGTTC
>3684109H1 HEANOT01 INCYTE
 ATTTCATCTTCAGGATTACAGTCATTCTGAANAGGAGAACATCAAACAAATTAGGAGTTGTGCAACAGCTCTTGT
 GAGGAGGCTAACGGACAGGAGAAAAGGTCTTCATCGTGGAAANAAATTAAATGTTTATTAAATAGATCACCAGCT
 GTTCAGAGTTACCATGTACGTATTCCACTAGCTGGTTCTGTATTCTCAGTTCTGATACGGCTTAGGGTAATGTG
 TACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCTTGT
>4713188H1 BRAIHT01 INCYTE
 CAAAGTTACTAAAAAAATACCACGAGGTCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCG
 ACAGTGGCCCTGGAGCACCAGTGGAGTGTGACTGTGTGCAAGGGAGCACAGGAGGAGAACCGATACCATTTCCTGCCAGGTTG
 CTCTGCCAGAGCTGTGCAAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCCTTATCTCCATCCTTAATCTCAGTT
 TTGCT
>458823H1 KERANOT01 INCYTE
 ANGAGTTGCCAGAGCTGTGCAAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCCTTATCTCCATCCTTAATCTCAGTT
 GTTTGNTTCAAGGACCTTCATCTCAGGATTACAGTCATTCTGAAAGAGGAGACATCAAACAGAACATTAGGAGTTG
 CAACAGCTTTGAGAGGAGGCTAACGGNCAGGAGAACAGGTTCTCAATCGTGGAAAGAAAATTAAATGTTTATTAA
 ATAGATC
>1303909H1 PLACNOT02 INCYTE
 AGAAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCCTCTGAACCTTCTAACAGAGGAGGTAACGATTATAC
 AGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAAGAACCTAAAGAGAACCGATACCATTTCCTGCCAGGGTGTCT
 CCTGGTTAACGCTGTGGGAACTGTGCCTGTTGTCCTCCACAATTGCAATGAATGTCAATGTGTCCCAGG

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FIG. 14 (CONTINUED).

>2739211H1 OVARNOT09 INCYTE
TGTCATTCTGAAAAGAGGAGACATCAAACAGAAATTAGGAGTTGTGCAACAGCTTTGAGAGGAGGCCAAAGGACAGGA
GAAAAGGTCTTCAATCGTGGAAAGAAAATTAAATGTTGATTAAATAGATCACCGACTAGTTCAGAGTTACCATGTACG
TATTCCACTAGCTGGGTCTGTATTCAGTTCTCGATAACGGCTTAGGTAATGTCAGTACAGGAAAAAACTGTGCAA
GTGAGCACCTGAT
>3325591H1 PTHYNOT03 INCYTE
TGCAACAGCTCTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAGTGGAAAGAAAATTAAATGTTGATT
AAATAGATCACCGACTAGTTCAGAGTTACCATGTACGTATTCACTAGCTGGGTCTGTATTCAGTTCTTCGATAACG
GCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTGCTAACCTAAAGCNCC
ATGTCNNGGCNAAAANCAGAAAAT
>3733565H1 SMCCNOS01 INCYTE
CCTTAATCTCAGTTGCTTCAGGACCTTCATCTCAGGATTTACAGTCAGTCATTCTGNAAGANGAGACATCAAACAG
AATTAGGNGTTGTGCAAAAGCTCTTTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTNCAATCGTGGAAAGNAAATT
AAATGTTGATNAAATNGATCACCGACTAGTTCAGAGTTACCATGTACGTATTCCACTAGCTGGNCNGTATTCACTCT
TTCGGAACGGCTTAGGTAATGTCAGTACAGGANAAAACTGTGCAAGTGAG
>3554223H1 SYNONOT01 INCYTE
ATTAATAGATCACCGACTAGTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTCTGTATTCAGTTCTTCGAT
ACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTGGCTTAACCTAAAG
CTCCATGTCCTGGCCTAAATCGTATAAAATCTGGATTTTNTTTTTTGCGCATATTCACATATGTAAACCAGN
ACATTCTATGTACNACAAACCTGGTTTAAAAAGAAC
>4507477H1 OVARDT01 INCYTE
GGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTCTGTATTCAGTTCTTCGATAACGGCTTAGGGTAAT
GTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTGGCTTAACCTAAAGCTCCATGTCCTGGGCC
TAAAATCGTATAAAATCTGGA
>4163378H1 BRSTNOT32 INCYTE
AATAGATCACCGACTAGTTCAGAGTTACCATGTACGTATTCCACTAGCTGGNTCTGTATTCAGTTCTTCGATAACG
GCTTAGGGTAATGTCAGTACAGGAAAAAGCTGTGCAAGTGAGCACCTGATTCCGTTGCCCTGGCTTAACCTAAAGCTCC
ATGTCCTGGCCTAAATCGTATA

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FIG. 15.

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>2054675H1 BEPINOT01 INCYTE
AAAGGAACATGTTGCTATGAATTAAACTTGTGTCGCTGATAGGACAGACTGGATTTCATATTCTTATAAATT
TCTGCCATTTAGAAGAAGAGAACTACATTATGGTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTATCTCACCT
TATCGATAAGTCAGTTATTTGTTCATTGTACATTTTATATTCTCCTTGACATTAACTGTTGGCTTTCTAA
TCTTGTAAATATATCTATTTTACCAAAGGTATTTAATATTCTTTTA
>3993180H1 LUNGNON03 INCYTE
CACAAATCACTCACCGACGTGGCCCTGGAGCACCAGGAGCTGACTGTGTGCAGAGGGAGCACAGGAGGATAGCC
GCATCACCACCAGCAGCTTGTCCCAGAGCTGAGCTGAGCTGATTCTATTAGAGAACGATGCTATCGTTATCTCCAT
CCTTAATCTCAGTTGTTGCTTCAGGACCTTCATCTCAGGATTACAGTCATTCTGAAAGAGGAGACATCAAACAG
AATTAGGAGTTGTCAACAGCTTTGAGAGGAGGCTAAAGGACAGGAGAANAGGTCTT
>3510192H1 CONCN0T01 INCYTE
TGCAGTGCAGTGGCTATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTGCTTCAGGACCTT
TCATCTCAGGATTACAGTCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTCAACAGCTCTTGAGAG
GAGGCCTAAAGGACAGGAGAAAAGGTCTTCAGTGGAAAGAAAATTAAATGTTGATTAAATAGATCACCAGCTAGTT
TCAGAGTTACCATGTACGTATCCACTAGCTGGTTCTGTATT
>4164633H1 BRSTNOT32 INCYTE
CTTGTAAATATATCTATTTTACCAAAGGTATTTAATATTCTTANTTATGACAACCTAGATCAACTATTTTAGCTTG
GTAATTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTTGACAAAATACATG
TATTCATTCTCGTATGGTCTAGAGTTAGATTATCTGCACTTAAACTGAATTGGAATAGAATTGGTAAGTTGCA
AAGACTTTGANAATAATTAAATTATCATATCTCCTTCAATTCTGTTATTGGGGAGAAAAT
>2559870H1 ADRETUT01 INCYTE
CACGAGGCTCTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCA
TGAGGAGTGTGACTGTGTGCAAGGGAGCACAGGGGATAGCCGATCACCACCAGCAGCTTGCCCAGAGCTGTG
AGTGCAGTGGCTGATCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTGCTTCAGGACCTTCA
TCTTCAGGATTACAGTCATTCTGAAAGAGGAGA
>3817470H1 BONSTUT01 INCYTE
TTAAAAGGAACATGTTGCTATGAATTAAACTTGTGTCATGCTGATAGGACAGACTGGATTTCATATTCTTATTAA
AATTCTGCCATTTAGAAGAAGAGAACTACATTATGGTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTATCTC
ACTTTATCGATAAGTCAGTTATTTGTTCATGTACATTATATTCTCCTTGACATTATAACTGTTGGCTTTC
TAATCTGTTAAATATATCTATTTTACCAAAGGTATTTAATATTCTT
>3979767H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATACCACCAAGCAGCTTGTCCCAGAGCTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATG
GTTATCTCCATCCTTAATCTCAGTTGTTGCTTCAGGACCTTCATCTCAGGATTACAGTCATTCTGAAAGAGGAG
ACATCAAACAGAATTAGGAGTTGTCAACAGCTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTTCATCGTG
GAAAGAANATTAAATGTTGATTAAATAGACACCAGCT
>3980011H1 LUNGTUT08 INCYTE
GGAGGATAGCCGCATACCACCAAGCAGCTTGTCCCAGAGCTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATG
GTTATCTCCATCCTTAATCTCAGTTGTTGCTTCAGGACCTTCATCTCAGGATTACAGTCATTCTGAAAGAGGAGA
CATCAAACAGAATTAGGAGTTGTCAACAGCTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTTCATCGTG
AAAGAAAATTAAATGTTGATTAAATAGATCACCA
>4825396H1 BLADDIT01 INCYTE
GAGAACCGATACCATTCTGGCCAGGTTGTCCTGGTAAACGCTGTTGGAACTGTGCCTGTTGTCACAAATT
GCAATGAATGTCAATGTGTCCAAGCAAAGTTACTAAAAAATACACAGGGCTCTCAGTTGAGACCAAGACCGGTG
AGGGGATTGACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTACTGTCAGGAGCACAG
AGGATAGCCGCATCACCAACCA
>3073703H1 BONEUNT01 INCYTE
AGAAAATCCAGAGTGGGATCTGAAACCTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTCTCAGT
GTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTCTGGCCAGGTTGTCCTGTTAACGCTGTTGGGAACT
GTGCTGTTGTCCTCACATTGCAATGAATGTCAATGTGTCCAAGCAAAGTTACTAAAAAATACACAGGGCTCTCAG
TTGAGACCAAGACCGGTGTCAGGGATTGACAAATCA
>862169H1 BRAITUT03 INCYTE
AGATGATAAAATATTGTTGCTCTGACA AAAAATACATGTATTCTCGTATGCTGCTAGAGTTAGATTAATCTGCA
TTTTAAAAAACTGAATTGGAATAGAATTGTTGAAAGACTTTGAAAATAATTAAATTATCATATCTCCATT
CTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATTCAAGATCCAGCCATTACTAACCTATTCTT
GGCGAAATCTCAGCCTAC
>4201385H1 BRAITUT29 INCYTE
TTTTAAAAAGGAACATGTTGCTATGAATTAAACTTGTGTCGCTGATAGGACAGACTGGATTTCATATTCTTAT
TAAATTTCTGCCATTAGAAGAGAACATACATTCACTGGTTGGAAGAGATAAACCTGAAAAGAAGAGTGGCCTATCT
TCACCTTATCGATAAGTCAGTTATTTGTTCATGTACATTCTCCTTGACATATAACTGTTGGCTTT

FIG. 15 (CONTINUED 1). 23/54

CTAATCTGTTAAATATCTATTACCAAGGTATTAATAT
 >1302516H1 PLACNOT02 INCYTE
 AGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTCCTCTGAACCTCTAACAGAGGAGGTAAAGATTATAC
 AGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAAGAACTAAAGAGAACCGATACCATTCTGCCAGGTTGCT
 CCTGGTTAACGCTGTGGTGGAACTGTGCCTGTTGTCCTCCACAATTGCAATGAATGTCATGTGCCCAGCAAAGTT
 ACTAAAAAAATACCACGAGGTCC
 >3684109H1 HEAANOT01 INCYTE
 ATTTCATCTCAGGATTACAGTCATTCTGAAANAGGAGAAATCAAACANAATTAGGAGTTGTGCAACAGCTCTTG
 GAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCATCGTGGAAANAAAATTAAATGTTGATTAATAGATCACCGAGCT
 GTTCAGAGTTACCATGTACGTATTCCACTAGCTGGTTCTGTATTCAGTTCTCGATACGGCTTAGGGTAATGTCAG
 TACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTGCTT
 >2549720H1 LUNGUT06 INCYTE
 TTAGCTTGGNAATTTCTAAACACAATTGTTAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAA
 AATACATGTATTCATTCTGTATGGTGCTAGAGTTAGATTAATCTGCATTAAAAAAACTGAATTGGAATAGAATTGG
 AAGTTGCAAAGACTTTGAAATAATTAAATTATCATATCTCCATTCTGTTATTGGAGATGAAAATAAAAGCAACT
 TATGANAGTAG
 >877279H1 LUNGAST01 INCYTE
 CTTTTTATGACAACTTAGATCAACTATTTAGCTTGGTAAATTTCTAAACACAATTGTTAGCCAGAGGAACAAA
 GATGATATAAAATATTGTTGCTCTGACAAAAACATGTATTCTCGATGGTCTAGAGTTAGATTAATCTGCAT
 TTTAAAAAAACTGAATTGGAATAGAATTGGTAAGTTGCAAAGGCTTTGAAAATAATTAAATTATCATATCTCCATTCC
 TGTTATTGGNGG
 >4713188H1 BRAIHCT01 INCYTE
 CAAAGTTACTAAAAAATACCACGAGGTCTTCAGTTGAGACCAAAGACCGGTCTCAGGGGATTGCACAAATCACTCACCG
 ACAGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCGAG
 CTCTTGCCCAGAGCTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCCATTCTCCATCTTAATCTCAGTTG
 TTGCT
 >2171082H1 ENDNOT03 INCYTE
 AGATAAACCTGAAAAGAAGAGTGGCCTTATCTCACTTATCGATAAGTCAGTTATTGTTCTATTGTCATTTA
 TATTCTCCTTTGACATTATAACTGTTGGCTTTCTAATCTGTTAAATATCTATTACCAAAAGGTATTTAATATT
 CTTTTTATGACAACCTAGATCAACTATTTAGCTTGGTAAATTTCTAAACACAATTGTTAGCCAGAGGAACAAA
 GATGA
 >875860H1 LUNGAST01 INCYTE
 CTGGATTTTCATATTCTTATTAACCTCTGCCATTAGAAGAAGAGAACTACATTCTAGGTTGGAAAGAGATAACCC
 TGGAAAAGAAGAGTGGCCTTATCTCACTTATCGATAAGTCAGTTATTGTTCTATTGTCACATTCTTATCTCCT
 TTGACATTATAACTGTTGGCTTTCTAATCTGTTAAATATCTATTACCAAAAGGTATTTAATATTCTTTTAT
 GAC
 >706168H1 SYNORAT04 INCYTE
 GCTCATATTCACATATGTAACACAGAACATCTATGTAACAAACCTGGTTTTAAAAAGGANCTATGTTGCTATGAAT
 TAAACTTGTGCGTGTGATAGGACAGACTGGATTTCATATTCTTATTAACCTCTGCCATTAGAAGAAGAGAAC
 TACATTCTAGGTTGGAAAGAGATAAAACCTGAAAAGAAGAGTGGCCTTATCTCANTTATCGATAAGTCAGTTATTG
 TTCA
 >458823H1 KERANOT01 INCYTE
 ANGAGTTGCCAGAGCTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCCATTCTGAAAGAGTGTG
 GTTGTGNTCAAGGACCTTCATCTCAGGATTACAGTCATTCTGAAAAGAGGAGACATCAAAACAGAATTAGGAGTTG
 CAACAGCTTTGAGAGGAGGCTAAAGGNCAAGGAGAAAAGGTCTCAATCGTGGAAAGAAAATAATGTTGATTAA
 ATAGATC
 >538436H1 LNODNOT02 INCYTE
 AAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTCAATTCTCGATGGTCTAGAGTTAGATTAATCTG
 CATTAAAAAAACTGAATTGGAATAGAATTGTTAAGTGTGCAAAGACTTTGAAAATAATTAAATTATCATATCTCCAT
 TCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATTCACTGAGCCATTACTAACCTAT
 >1303909H1 PLACNOT02 INCYTE
 AGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTCCTCTGAACCTCTAACAGAGGAGGTAAAGATTATAC
 AGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAAAGAACTAAAGAGAACCGATACCATTCTGCCAGGTTGCT
 CCTGGTTAACGCTGTGGTGGAACTGTGCCTGTTGTCCTCCACAATTGCAATGAATGTCATGTGCCCAGG
 >2739211H1 OVARNOT09 INCYTE
 GTGCATTCTGAAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTTGTGAGAGGAGGCCTAAAGGACAGGA
 GAAAAGGTCTCAATCGTGGAAAGAAAATTAAATGTTGATTAATAGATCACAGCTAGTTCAAGGTTACCATGTAC
 TATTCCACTACCTGGTTCTGTATTCAGTTCTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTGTGCCA
 GTGAGCACCCTGAT

FIG. 15 (CONTINUED 2). 24/54

>2550343H1 LUNGUT06 INCYTE
TGTACATTTTATATTCTCCTTGCACATTATAACTGTTGGCTTTCN~~A~~TCTGTTAAATATATCTATTTTACCAAAG
GTATTTAATATTCTTTTATGACAACCTAGATCAACTATTTAGCTGGAAATTCTAAACACAATTGTTAGC
CAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTCATTCTCGTATGGTGCTA
>5321148H1 FIBPFEN06 INCYTE
CACAAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGNCAAAAATACATGTATTCATTCTCGTA
TGGTGCTAGAGTTAGATTAATCTGCATTTAAAAACTGAATTGAAATAGAATTGGAAGACTTTGAAA
TAATTAAATATCATATCTCCATTCTGTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAATTCAAGATCCAC
CATTACTAAC
>879495H1 THYRNOT02 INCYTE
ATTCATTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTAAAAACTGAATTGAAATAGAATTGGAAGACTT
AGACTTTGAAAATAATTAAATTATCATATCTCCATTCTGTATTGGAGATGAAAATAAAAGCAACTTATGAAAGT
AGACATTCAAGATCCAGCATTACTAACCTATTCTTTGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCT
TGAAAAA
>3325591H1 PTHYNOT03 INCYTE
TGCAACAGCTTTGAGAGGAGGCCAAAGGACAGGAGAAAAGGTCTTCAATCGGAAAGAAAATTAAATGTTGATT
AAATAGATCACCAGCTAGTTTAGAGTTACCATGTACGTATTCCACTAGCTGGTTCTGTATTCAGTTCTTCGATACG
GCTTAGGGTAATGTCAGTACAGGAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTGCTTAACCTAAAGCNCC
ATGTCNNGGCNAAAANCAGAAAAT
>543890H1 OVARNOT02 INCYTE
TTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAATACATGTATTC
TTCTCGTATGGTGCTAGAGTTAGATTAATCTGCATTTAAAAACTGAATTGNAATAGAATTGGAAGACTT
TTGAAAATAATTAAATTATCATATCTCCATTCTGTATTGGAGGATGAAAATAAAAGCAACTTATGAAAGTAGG
ACATTCAAGATC
>3733565H1 SMCCNOS01 INCYTE
CCTTAATCTCAGTTGTTGCTCAAGGACCTTCATCTCAGGATTACAGTCATTCTGNAAGANGAGACATCAAACAG
AATTAGGNNTTGTGCAAAAGCTTTGAGAGGAGGCCAAAGGACAGGAGAAAAGGTCTNCAATCGGAAAGNAAATT
AAATGTTGATNAAATNGATCACCAGCTAGTTTAGAGTTACCATGTACGTATTCCACTAGCTGGNCNGTATTCA
TCGGAACGGCTTAGGGTAATGTCAGTACAGGAAAATGTGAGT
>4641939H1 PROSTMT03 INCYTE
GTACTACAAACCTGGTTTAAAAAGGAACATGTTGCTATGAAATTAAACTGTTGTCATGCTGATAGGACAGACTGGAT
TTTNCATATTCTTATTAAATTCTGCCATTAGAAGAGAACTACATTCATGGTTGGNAGAGATAAACCTGAAA
GAAGAGTGGCCTTATCTCACTTTATCGATAAGTCAGTTATTGTTCATGTCATTTTATATTCTCCTTGACAT
ATAACGTGGCTTT
>2007780H1 TESTNOT03 INCYTE
TTATATTCTCCTTTGACATTATAACTGTTGGCTTTCTAATCTGTTAAATATATCTATTTTACCAAAGGTATTAAT
ATTCTTTTATGACAACCTAGATCAACTATTTTAGCTGGAAATTCTAAACACAATTGTTATGCCAGAGGAAC
AAAGATGATATAAAATATTGTTGCTCTGANAACATGTAT
>3085331H1 HEAONOT03 INCYTE
GCTCATATTCACATATGTAACCAACAGAACATTCTATGTAACCAACCTGGTTTAAAAAGGAACATTTGCTATGAAATT
AAACTTGTGCGTGTGATAGGACAGACTGGNTTTCTATTTCTTATTANAATTCTGCCATTAGAAGAGAACTA
CATTCACTGGTTGGAAGAGATAAACCTGAAAAGAGACTGGCCTATTCACTTATCGATAAGTCAGT
>3414043H1 PTHYNOT04 INCYTE
GCTCATATTCACATATGTAACCAACAGAACATTCTATGTAACCAACCTGGTTTAAAAAGGAACATGTTCTATGAAAT
TAAACTTGTGCGTGTGATAGGACAGACTGGATTTCATATTCTTATTAAATTCTGCCATTAGAAGAGAGAAC
TACATTCACTGGTTGGAAGAGATAAACCTGAAA
>3705963H1 PENCNOT07 INCYTE
ANACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTGCTAACTCTAAAGCTCCATGTCCTGGGCCTAAATCGTATAAAA
TCTGGAnnnnnnnnnnnnnnnnnnnnGCTCATATTCACTATGTAACCAACAGAACATTCTATGTAACCAACCTGGTTTTA
AAAAGGAACATGTTGCTATGAAATTAAACTGTCGCTGATAGGACAGACTGGATTTCATATTCTTATTAAAGANGGG
TTCTGCCATTAGAAGAGAGAACTACNTTCAGGTTGGAAGAGATAACCTGAAAGANGGG
>5137051H1 OVARDIT04 INCYTE
AAAAAACTGAAATTGGAATAGAATTGGAAGACTTGTGAAAGACTNTTGTAAAATAATTAAATTATCATATCTCCATTCTGT
TATTGAGATGAANATAAAAAGCAACTTATGAAAGTAGACATTCACTGACATCCAGCCATTACTAACCTATTCTTTTCCGG
AAATCTGACCCCTAGCTCAGAAAACATAAAGCACCTGAAAAGACTTGGCAGCTCCTGATAAAAGCGTGTNTGTCA
GTAGGAACACATCCTATTATTGTCAGTGTGTTATTAT
>3554223H1 SYNONOT01 INCYTE
ATTAATAAGATCACCAGCTAGTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTCGAT
ACGGCTTAGGGTAATGTCAGTACAGGAAAAGACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTGGCTTAACCTAAAG

FIG. 15 (CONTINUED 3). 25/54

CTCCATGTCCTGGCCTAAAATCGTATAAAATCTGGATTTTTNTTTTGCGCATATTACACATATGTAAACCAGN
ACATTCTATGTACNACAAACCTGTTTAAAGGAAC
>4507477H1 OVARTDT01 INCYTE
GGCTAGTTAGAGTTACCATGTACGTATCCACTAGCTGGGTTCTGTATTCAGTTCTTCGATACGGCTTAGGGTAAT
GTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTGCTTAACCTAAAGCTCCATGTCCTGGGCC
TAAAATCGTATAAAATCTGGA
>1955646H1 CONNNOT01 INCYTE
TGGTAAGTTGCAAAGACTTTGAAAATAATTAAATTATCATATCTTCATTCCTGTTATTGGAGATGAAAATAAAAGC
AACTTATGAAAGTAGACATTCACTAGCATTACTAACCTATTCCCTTTGGGAAATCTGAGCCTAGCTCAGAAAA
ACATAAAGCACCTGAAAAAGACTTGGCAGCTCCTGATAAAAGCGTGTGCTGTGAGTAGGAAACACATCCTATTAA
TTGTGATGTTGTTATATCCTAAACC
>4163378H1 BRSTNOT32 INCYTE
AATAGATCACCAGCTAGTTAGAGTTACCATGTACGTATCCACTAGCTGGGNTCTGTATTCAGTTCCCTTCGATACG
GCTTAGGGTAATGTCAGTACAGGAAAAAGCTGTGCAAGTGAGCACCTGATTCCGTTGCCTGCTTAACCTAAAGCTCC
ATGTCCTGGCCTAAAATCGTATA
>5095141H1 EPIMNON05 INCYTE
AGATAAAACCTGAAAAGAGTGGCCTTATNTTCACTTTATCGATAAGTCAGNTTATTGTTCAATTGTCACATTNNNA
TATTCTCCTTTGACATTATACTGNTGGCTTTCTAACNCNTGTTAAATATATCTATTACCAAAAGGTATTAAATATT
CTTT
>943826H1 ADRENOT03 INCYTE
TATGGTGCTAGAGTTAGATTAATCTGCATTAAAAACTGAATTGGAATAGAATTGTAAGTTGCAAAGACTTTGAA
AATAATTAAATTATCATATCTTCATTCCTGTTATTGGAGATGAAAATAAAAGCAACTTATG
>3451273H1 UTRSNON03 INCYTE
TTTTTNTTTGCTCATATTACATATGTAACCNGAACATTCTATGTACNACAAACCTGGTTTAAAAGGAACATATG
TTGCTATGAATTAAACTTGTGCTGTGCTGATAGGACAGACTGGATTTCANATTCTTANTAAANNTTCTGCCATTAG
AAGA
>1402278H1 LATRTUT02 INCYTE
GTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTGCTTAACCTAAAGCTCCATGTCCTGGCCTAAA
ATCGTATAAAATCTGGAnnnnnnnnnnnnnnnnnnGCTCATATTACATATGTAACCAACATTCTATGTACTACAAA
CCTGGTTTAAAAGGAACATATGTTGCTATGAATTAAACTTGTGCTGTGCTGATAGGACAGACTGGATTTCATATT
CTTA
>4361191H1 SKIRNOT01 INCYTE
GCAAAGACTTTGANAATNATTAANTTATCATATCTCCATTCTGTTATNGGAGATGANAATAAAAAGCAACTTATGA
AACTAGACATTCACTGAGCCATTACTAACCTATTCTTTGGGAAATCTGAGCCTAGCNCAGAAAAACATAAAGC
ACCTTGAAAAGACTTGGCAGCTCCTGATAAAAGCGTGTGCTGTGAGTAGGAACACATCCNATTATTGNTGNTGN
GNGGTTTATGATC
>1307017H1 PLACNOT02 INCYTE
TGTCACTAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTGCTTAACCTAAAGCTCCATGTCCTGGC
CTAAAATCGTATAAAATCTGGAnnnnnnnnnnnnnnGCTCATATTACATATGTAACCAACATTCTATGTACT
ACAAACCTGGTTTAAAAGGAACATATGTTGCTATGAATTAAACTTGTGCTGTGCTGATAGGACAGACTGGATTTC
TAT
>5032225H1 HEARFET03 INCYTE
AATTATCATATCTCCATTCTGTTATTGGAGATGNAATAAAAAGCAACTTATGAAAGTAGACATTCACTGAGCCAT
TACTAACCTATTCTTTGGGAAATCTGAGCCTAGCTCAGA-AAAACATAAAAGCACCTTGAAAAGACTGTCAGCTC
CTGATAAAAGCGTGTGCTGTGAGTAGGAACACATCCATTATTGTGATGTTGGTTTATTATCTAAACTCGTT
CCAT
>3732621H1 SMCCNOS01 INCYTE
ANAGATGATATAAAANATTGTCCTGACAANNATACATGTATTCATTCTCGTATGGCTAGAGTTAGATTAACTG
CNTTTAAAAAAACTGANTTGAATAGANTGGTAAGTGCAGNCNTTGAAAATNATTAAGTATCAGAT
>3530274H1 BLADNOT09 INCYTE
TTCCATTCCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATTCACTGAGCCATTACTAACCTATT
CCTTTTTGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAAGCACCTTGAAAAGACTGGCAGCTCCTGATAAGCG
TGCTGTGCTGTGAGTAGGAACACATCCATTATTGTGATGTTGGTTTATTATCTAAACTCTGTTCCATACACTG
TATAAATACATGGATATTGTACAGAAGTATGTCCTTAACCAGTTCA
>3530249H1 BLADNOT09 INCYTE
CTTCATTCCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGANAGTAGACATTCACTGAGCCATTACTAACCTATT
TCCTTTTTGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAAGCACCTTGAAAAGACTGGCAGCTCCTGATAAGCG
GTGCTGTGCTGTGAGTAGGAACACATCCATTATTGTGATGTTGGTTTATTATCTAAACTCTGTTCCATACACT
TGTATAAATACATGGATATTGTACAGAAGTATGTCCTTAACCAGTTCACTTATTGTACCTGG

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FIG. 16.

VEGFE1	AAAATGTATGGATACAACTTAC	22
VEGFE2	GTTTGATGAAAGATTGGGCTTG	23
VEGFE3	TTTCTAAAGGAAATCAAATTAG	22
VEGFE4	GATAAGATTGTATCTGATG	20
VEGFE5	GATGTCTCCTCTTCAG	17
VEGFE6	GCACAACTCCTAATTCTG	18
VEGFE7	AGCACCTGATTCCGTTGC	19
VEGFE8	TAGTACATAGAATGTTCTGG	20
VEGFE9	AAGAGACATACTTCTGTAC	19
VEGFE10	CCAGGTACAATAAGTGAAC TG	21

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FIG. 17.

+3
N L L T E E V R L Y M N I F L L

]

1 AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTTCTTCTG
AACCTTCTAA CAGAGGAGGT AAGATTATAC
TCCTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC
TTGGAAGATT GTCTCCTCCA TTCTAATATG

+3 S C T P R N F S V S I R E E L K R
T D T I F W P G C L
-----]

81 AGCTGCACAC CTCGTAACCT CTCAGTGTCC ATAAGGAAAG AACTAAAGAG
AACCGATACC ATTTCTGGC CAGGTTGTCT
TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCCTTC TTGATTTCTC
TTGGCTATGG TAAAAGACCG GTCCAACAGA

-2

+3 L V K R C G G N C A C C L H N C N
E C Q C V P S K V

161 CCTGGTTAAA CGCTGTGGTG GGAACGTGCTC CTGTTGTCTC CACAATTGCA
ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
GGACCAATTG GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT
TACTTACAGT TACACAGGGT TCGTTCAAT

-2

+3 T K K Y H E V L Q L R P K T G V R
G L H K S L T D V A

+1
D C T N H S P T W P V S G
-----]

241 CTAAAAAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC CGGTGTCAAGG
GGATTGCACA AATCACTCAC CGACGTGGCC
GATTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTCTG GCCACAGTCC
CCTAACGTGT TTAGTGAGTG GCTGCACCGG

-2
-----[

+3 L E H H E E C D C V C R G S T G G

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FIG. 17 (CONTINUED).

>

+2	I A A S P P A A L A	V Q R E H R R
		-----]

+1 W S T M R S V T V C A E G A Q E D

S R I T T S S S C	
-------------------	--

321 CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG
 ATAGCCGCAT CACCACCAGC AGCTCTTGC
 GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCCCTCC
 TATCGCGTA GTGGTGGTCG TCGAGAACGG

+2 Q S C A V Q W L I L L E N V C V I	
S I L N L S C L L Q	

+1 P E L C S A V A D S I R E R M R Y

L H P	
-------	--

----->

401 CAGAGCTGTG CAGTCAGTG GCTGATTCTA TTAGAGAACG TATGCCTTAT
 CTCCATCCTT AATCTCAGTT GTTGCTTCA
 GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA
 GAGGTAGGAA TTAGAGTCAT CAAACGAAGT

+2 G P F I F R I Y S A F	
--------------------------	--

----->

481 AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC
 AAACAGAATT AGGAGTTGTG CAACAGCTCT
 TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTTC TCCTCTGTAG
 TTTGTCTTAA TCCTCAACAC GTTGTGAGA

561 TTTGAGAGGA GCCCTAAAGG ACAGGAGAAA AGGTCTCAA TCGTGGAAAG
 AAAATTAAAT GTTGTATTAA ATAGATCACC
 AAACTCTCCT CCGGATTTC TGTCCTCTT TCCAGAAGTT AGCACCTTTC
 TTTTAATTAA CAACATAATT TATCTAGTGG

641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCTGTAT
 TTCAGTTCTT TCGATACGGC TTAGGGTAAT
 TCGATCAAAG TCTCAATGGT ACATGCCATA GGTGATCGAC CCAAGACATA
 AAGTCAAGAA AGCTATGCCG AATCCCATT

721 GTCAGTACAG GAAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTGCCTT
 GGCTTAACTC TAAAGCTCCA TGTCCTGGGC
 CAGTCATGTC CTTTTTTGTA CACGTTCACT CGTGGACTAA GGCAACGGAA
 CGGAATTGAG ATTCGAGGT ACAGGACCCG

801 CTAATCGT ATAAATCTG GA
 GATTTAGCA TATTTAGAC CT

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FIG. 18.

+3
N L L T E E V R L Y M N I F L L
] -----

1 AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTTCTTCTG
AACCTTCTAA CAGAGGAGGT AAGATTATAC
TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC
TTGGAAGATT GTCTCCTCCA TTCTAATATG
+3 S C T P R N F S V S I R E E L K R
T D T I F W P G C L] -----

81 AGCTGCACAC CTCGTAACCTT CTCAGTGTCC ATAAGGAAAG AACTAAAGAG
AACCGATACC ATTTCTGGC CAGGTTGTCT
TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCCTTC TTGATTCTC
TTGGCTATGG TAAAAGACCG GTCCAACAGA
-2 <-----

+3 L V K R C G G N C A C C L H N C N
E C Q C V P S K V -----

161 CCTGGTTAAA CGCTGTGGTG GGAACTGTGC CTGTTGTCTC CACAATTGCA
ATGAATGTCA ATGTGTCCC AGCAAAGTTA
GGACCAATTT GCGACACCAC CCTTGACACG GACAACAGAG GTGTTAACGT
TACTTACAGT TACACAGGGT TCGTTCAAT
-2 -----

+3 T K K Y H E V L Q L R P K T G V R
G L H K S L T D V A -----

+1 V S G
D C T N H S P T W P] -----

241 CTAAAAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC CGGTGTCAGG
GGATTGCACA AATCACTCAC CGACGTGGCC
GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTCTG GCCACAGTCC
CCTAACGTGT TTAGTGAGTG GCTGCACCGG

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FIG. 18 (CONTINUED 1).

-2

+3 L E H H E E C D C V C R G S T G G

>
+2
I A A S P P A A L A V Q R E H R R
]-----
+1 W S T M R S V T V C A E G A Q E D
S R I T T S S S C

321 CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG
ATAGCCGCAT CACCACCAAGC AGCTCTTGC
GACCTCGTGG TACTCCTCAC ACTGACACAC ACGTCTCCCT CGTGTCCCTCC
TATCGGCGTA GTGGTGGTCG TCGAGAACGG
+2 Q S C A V Q W L I L L E N V C V I
S I L N L S C L L Q

+1 P E L C S A V A D S I R E R M R Y
L H P
----->
401 CAGAGCTGTG CAGTCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT
CTCCATCCTT AATCTCAGTT GTTGCTTC
GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA
GAGGTAGGAA TTAGAGTCAA CAAACGAAGT
+2 G P F I F R I Y S A F
----->
481 AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC
AAACAGAATT AGGAGTTGTG CAACAGCTCT
TCCTGGAAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC TCCTCTGTAG
TTTGTCTTAA TCCTCAACAC GTTGTGAGA
561 TTTGAGAGGA GGCTAAAGG ACAGGAGAAA AGGTCTCAA TCGTGGAAAG
AAAATTAAT GTTGTATTAA ATAGATCACC
AAACTCTCCT CC GGATTTCC TGT CCTCTTT TCCAGAAGTT AGCACCTTTC
TTTTAATTAA CAACATAATT TATCTAGTGG
641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CC ACTAGCTG GGTCTGTAT
TTCAGTTCTT TCGATACGGC TTAGGGTAAT
TCGATCAAAG TCTCAATGGT ACATGCCATAA GGTGATCGAC CCAAGACATA
AAGTCAAGAA AGCTATGCCG AATCCCATT
721 GTCAGTACAG GAAAAAAACT CTGCAAGTGA GCACCTGATT CC GTTGCCTT
GGCTTAACTC TAAAGCTCCA TGT CCTGGGC

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FIG. 1B (CONTINUED 2).

CAGTCATGTC CTTTTTTGA CACGTTCACT CGTGGACTAA GGCAACGGAA
CCGAATTGAG ATTCGAGGT ACAGGACCCG

801 CTAAAATCGT ATAAAATCTG GATTTTTTN TTTTTTTTG CGCATATTCA
CATATGTAAA CCAGAACATT CTATGTACTA
GATTTTAGCA TATTTAGAC CTAAAAAAAN AAAAAAAAAC GCGTATAAGT
GTATACATTT GGTCTTGTAA GATACATGAT

881 CAAACCTGGT TTTTAAAAAG GAACTATGTT GCTATGAATT AAACTTGTGT
CGTGCTGATA GGACAGACTG GATTTTCAT
GTTTGGACCA AAAATTTTC CTTGATACAA CGATACTTAA TTTGAACACA
GCACGACTAT CCTGTCTGAC CTAAAAAGTA

-3

<-----

961 ATTTCTTATT AAAATTTCTG CCATTTAGAA GAAGAGAACT ACATTCATGG
TTTGGAAAGAG ATAAACCTGA AAAGAAGAGT
TAAAGAATAA TTTTAAAGAC GGTAAATCTT CTTCTCTTGA TGTAAGTACC
AAACCTTCTC TATTGGACT TTTCTTCTCA

-3

<-----

1041 GGCCTTATCT TCACCTTATC GATAAGTCAG TTTATTTGTT TCATTGTGTA
CATTTTATA TTCTCCTTT GACATTATAA
CCGGAATAGA AGTGAATAG CTATTCAGTC AAATAAACAA AGTAACACAT
GTAAAAATAT AAGAGGAAAA CTGTAATATT

-3

-----[

1121 CTGTTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTA CCAAAGGTAT
TTAATATTCT TTTTTATGAC AACTTAGATC
GACAACCGAA AAGATTAGAA CAATTTATAT AGATAAAAAT GGTTCCATA
AATTATAAGA AAAAATACTG TTGAATCTAG

1201 AACTATTTT AGCTTGGTAA ATTTTCTAA ACACAATTGT TATGCCAGA
GGAACAAAGA TGATATAAAA TATTGTTGCT
TTGATAAAAA TCGAACCAATT TAAAAAGATT TGTGTTAACCA ATATCGGTCT
CCTTGTCTTCT ACTATATTT ATAACAAACGA

1281 CTGACAAAAA TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA
ATCTGCATTT TAAAAAACTG AATTGGAATA
GACTGTTTT ATGTACATAA AGTAAGAGCA TACCACGATC TCAATCTAAT
TAGACGTAAA ATTTTTGAC TTAACCTTAT

1361 GAATTGGTAA GTTGCAGA CTTTTGAAA ATAATTAAAT TATCATATCT
TCCATTCCCTG TTATTGGAGA TGAAAATAAA
CTTAACCATT CAACGTTCT GAAAAACTTT TATTAATTAA ATAGTATAGA
AGGTAAGGAC AATAACCTCT ACTTTTATTT

1441 AAGCAACTTA TGAAAGTAGA CATTCAAGATC CAGCCATTAC TAACCTATTG
CTTTTTGGG GAAATCTGAG CCTAGCTCAG
TTCGTTGAAT ACTTTCTATC GTAAGTCTAG GTCGGTAATG ATTGGATAAG
GAAAAAAACCC CTTTAGACTC GGATCGAGTC

*32/54**FIG. 18 (CONTINUED 3).*

1521 AAAAACATAA AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT
GCTGTGCTGT GCAGTAGGAA CACATCCTAT
TTTTGTATT TCGTGGAACT TTTTCTGAAC CGTCGAAGGA CTATTCGCA
CGACACGACA CGTCATCCTT GTGTAGGATA

1601 TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTT CATAACACTTG
TATAAAATACA TGGATATTTT TATGTACAGA
AATAACACTA CAACACCAAA ATAATAGAAT TTGAGACAAG GTATGTGAAC
ATATTTATGT ACCTATAAAA ATACATGTCT

1681 AGTATGTCTC TTAACCAGTT CACTTATTGT ACCTGG
TCATACAGAG AATTGGTCAA GTGAATAACA TGGACC

FIG. 19. DNA and polypeptide sequence used for mammalian cell expression 33/54

+1 m s 1 f g 1 1 1 1 t s a l a g q r
1 GGATCCAAAA TGAGCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC CGGCCAGAGA

+1 q g t q a E S N L S S K F Q F S S N K E
61 CAGGGGACTC AGGCAGAAC CAACCTGAGT AGTAATTCC AGTTTCCAG CAACAAGGAA

+1 Q N G V Q D P Q H E R I I T V S T N G S
121 CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGCTGTAC TAATGGAAGT

+1 I H S P R F P H T Y P R N T V L V W R L
181 ATTACACAGCC CAAGGTTTC TCATACTTAT CCAGAAATA CGGTCTTGGT ATGGAGAGTTA

+1 V A V E E N V W I Q L T F D E R F G L E
241 GTAGCAGTAG AGAAAATGT ATGGATACAA CTTACGTTG ATGAAAGATT TGGGCTTGAA

+1 D P E D D I C K Y D F V E V E E P S D G
301 GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC CAGTGATGCA

+1 T I L G R W C G S G T V P G K Q I S K G
361 ACTATATTAG GCGCTGGTG TGTTCTGGT ACTGTACCAAG GAAACAGAT TTCTAAAGGA

+1 N Q I R I R F V S D E Y F P S E P G F C
421 AATCAAATTAA GGATAAGATT TGTATCTGAT GAATATTTC CTTCTGAACC AGGGTTCTGC

+1 I H Y N I V M P Q F T E A V S P S V L P
481 ATCCACTACA ACATGTCTGCCACACAATTC ACAGAAGCTG TGAGCTCTTC AGTGCTACCC

+1 P S A L P L D L L N N A I T A F S T L E
541 CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTAG TACCTTGAA

+1 D L I R Y L E P E R W Q L D I E D L Y R
601 GACCTTATTTC GATATCTTGA ACCAGAGAGA TGGCAATTGG ACTTAAAGA TCTATATAGG

+1 P T W Q L L G K A F V F G R K S R V V D
661 CCAACTTGGC AACCTCTTGG CAAGGCTTTT GTTTTGAA GAAACAGATCCAG AGTGGTGGAT

+1 L N L L T E E V R L Y S C T P R N F S V
721 CTGAACCTTC TACAGAGGA GGTAAGATTAA TACAGCTGCA CACCTCGTAA CTTCTCAGTG

+1 S I R E E L K R T D T I F W P G C L L V
781 TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTCT GGCCAGGTG TCTCTCTGGTT

+1 K R C G G N C A C C L H N C N E C Q C V
841 AAACGCTGTG TGCGCAACTG TGCCTGTTGT CTCCACAATT GCAATGAATG TCAATGTGTC

+1 P S K V T K K Y H E V L Q L E P K T G V
901 CCAAGCAAGG TTACTAAAAA ATACCACGAG GCGCTTCAGT TGAGACCAAA GACCGGTGTC

+1 R G L H K S L T D V A L E H H E E C D C
961 AGGGGATTGC ACATCACT CACCGACGTG GCCCTGGAG ACCATGAGGA GTGTGACTGT

+1 V C R G S T G G S R G P F E G K P I P N
1021 GTGTGCAAGAG GGAGCACAGG AGGATCTAGA GGGCCCTTG AAGGTAGGCC TATCCCTAAC

+1 P L L G L D S T R T G H H H H H H H
1081 CCTCTCTCG GTCTGATTC TAGCGCTTACG CGTCATGATG ACCATGACCA TTGA

FIG. 20. DNA and polypeptide sequence used for baculovirus/insect cell expression 34/54

1 GAATTCAAAG GCCTGTATTT TACTGTTTC GTAACAGTTT TGTAATAAAA AAACCTATAA

+3 m k f l v n v a l v f m v v y i s y i
61 ATATGAAATT CTTAGTCAAC GTGCCCTTG TTTTATGGT CGTATACATT TCTTACATCT

+3 y a D P E S H H H H H E S N L S S K F
121 ATGGGGATCC CGAGTCTCAC CATCACCACC ATCATGAATC CAACCTGAGT AGTAAATTCC

+3 Q F S S N K E Q N G V Q D P Q H E R I I
181 AGTTTCCAG CAACAAGGAA CAGAPCGGAG TACAAGATCC TCAGCATGAG AGAATTATTA

+3 T V S T N G S I H S P R F P H T Y P R N
241 CTGTGTCTAC TAATGGAAGT ATTACAGGCC CAAGGTTCC TCATACTTAT CCAAGAAATA

+3 T V L V W R L V A V E E N V W I Q L T F
301 CGGTCTTGGT ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTG

+3 D E R F G L E D P E D D I C K Y D F V E
361 ATGAAAGATT TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG

+3 V E E P S D G T I L G R W C G S G T V P
421 TTGAGGAACC CAGTGATGGA ACTATATTAG GGCGCTGGT TGGTCTGGT ACTGTACCAAG

+3 G K Q I S K G N Q I R I R F V S D E Y F
481 GAAAACAGAT TTCTAAAGGA AATCAATTAA GGATAAGATT TGTATCTGAT GAATATTTTC

+3 P S E P G F C I H Y N I V M P Q F T E A
541 CTTCTGAACC ACCGTTCTGC ATCCACTACA ACATTGTCAAT GCCACAATT ACAGAAGCTG

+3 V S P S V L P P S A L P L D L L N N A I
601 TGAGTCCTTC AGTCCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA

+3 T A F S T L E D L I R Y L E P E R W Q L
661 CTGCCTTAG TACCTTGAA GACCTTATTC GATATCTGAA ACCAGAGAGA TGGCAGTTGG

+3 D L E D L Y R P T W Q L L G K A F V F G
721 ACTTACAAGA TCTATATAGG CCAACTTGGC AACTTCTGG CAAGGCTTTT GTTTTGAA

+3 R K S R V V D L N L L T E E V R L Y S C
781 GAAAATCCAG ATGCGTGGAT CTGAACTTTC TAAACAGAGGA GGTAAGATTA TACAGCTGCA

+3 T P R N F S V S I R E S L K R T D T I F
841 CACCTCGTAA CTCTCACTG TCCATAGGG AAGAACTAAA GAGAACCGAT ACCATTTCT

+3 W P G C L L V K R C G G N C A C C L H N
901 GGCCAGGTTG TCTCTGGTT AAGCCGTGTG GTGGAACTG TCCCTGTTCT CTCCACAAATT

+3 C N E C Q C V P S K V T K K Y H E V L Q
961 GCAATGAATG TCAATGTGTC CCAACCAAAG TTACTAAAAA ATACCACGAG GTCCTTCAGT

+3 L R P K T G V R G L H K S L T D V A L E
1021 TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAAACTCACT CACCGACGTG GGCCTCGAGC

+3 H H E E S D C V C R G S T G G
1081 ACCATGAGGA GTGTGACTGT CTGTGAGAG GGAGCACAGG AGGATAGCTC TAGA

FIG. 21. DNA and polypeptide sequence used for *E.coli* expression 35/54

+3 Q T N S S S N N N N N N N N N N L G I
 1 CGCAGACTAA TTCGAGCTCG AACACAACA ACAATAACAA TAACAACAAC CTCGGGATCG

+3 E G R I S E F E S N L S S K F Q F S S N
 61 AGGAAGGAT TTCAAGATTG GAATCCAACC TGAGTAGTAA ATTCCAGTTT TCCAGCAACA

+3 K E Q N G V Q D P Q H E R I I T V S T N
 121 AGGAACAGAA CGGAGTACAA GATCCTCAGC ATGAGAGAAT TATTACTGTG TCTACTAATG

+3 G S I H S P R F P H T Y P R N T V L V W
 181 GAAGTATTCA CAGCCCAAGG TTTCTCATA CTTATCCAAG AAATACGGTC TTGGTATGGA

+3 R L V A V E E N V W I Q L T F D E R F G
 241 GATTAGTAGC AGTAGAGGAA AATGTATGGA TACAACCTAC GTTGATGAA AGATTTGGC

+3 L E D P E D D I C K Y D F V E V E E P S
 301 TTGAAGACCC AGAAGATGAC ATATGCAAGT ATGATTTGT AGAAGTTGAG GAACCCAGTG

+3 D G T I L G R W C G S G T V P G K Q I S
 361 ATGAACTAT ATTAGGGCGC TGGTGTGGTT CTGGTACTGT ACCAGGAAA CAGATTCTA

+3 K G N Q I R I R F V S D E Y F P S E P G
 421 AAGGAAATCA AATTAGGATA AGATTTGTAT CTGATGAATA TTTCCCTCT GACCCAGGGT

+3 F C I H Y N I V M P Q F T E A V S P S V
 481 TCTGCATCCA CTACAACATT GTCATGCCAC AATTACAGA AGCTGTGAGT CCTTCAGTGC

+3 L P P S A L P L D L L N N A I T A F S T
 541 TACCCCCCTTC AGCTTGCCA CTGGACCTGC TTAATAATGC TATAACTGCC TTTAGTACCT

+3 L E D L I R Y L E P E R W Q L D L E D L
 601 TGGAAGACCT TATTCGATAT CTTGAACAG AGAGATGGCA GTTGGACTTA GAAGATCTAT

+3 Y R P T W Q L L G K A F V F G R K S R V
 661 ATAGGCCAAC TTGGCAACTT CTTGGCAAGG CTTTGTTTT TGGAAGAAA TCCAGAGTGG

+3 V D L N L L T E E V R L Y S C T P R N F
 721 TGGATCTGAA CCTTCTAACCA GAGGAGGTA GATTACAG CTGCACACCT CGTAACCTCT

+3 S V S I R E E L K R T D T I F W P G C L
 781 CAGTGTCCAT AAGGAAAGAA CTAAGAGAA CCGATACCAT TTTCTGCCA GGTTGTCTCC

+3 L V K R C G G N C A C C L H N C N E C Q
 841 TGGTAAACG CTGTGGTGGG AACTGTGCCT GTTGTCTCCA CAATTGCAAT GATGTCAAT

+3 C V F S K V T K K Y H E V L Q L R P K T
 901 GTGTCCCAG CAAAGTTACT AAAAATACC ACAGGGTCCT TCAGTTGAGA CCAAAGACCG

+3 G V R G L H K S L T D V A L E H H E E C
 961 GTGTCAAGGG ATTGCACAAA TCACTCACCG ACAGGGCCCT GGAGCACCAC GAGGAGTGTG

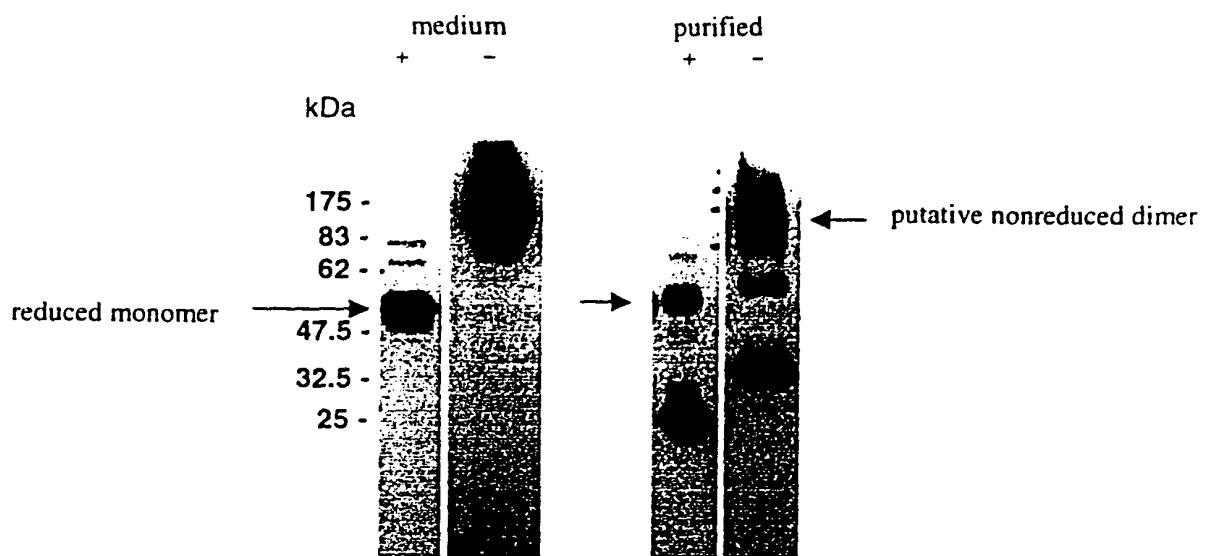
+3 D C V C R G S T G G H H H H H H *
 1021 ACTGTGTGTG CAAAGGGAGC ACAGGAGGAC ATATCACCA TCACCATG ACTAGAGTCG

1081 AJCTGCAGGC AAGCTT

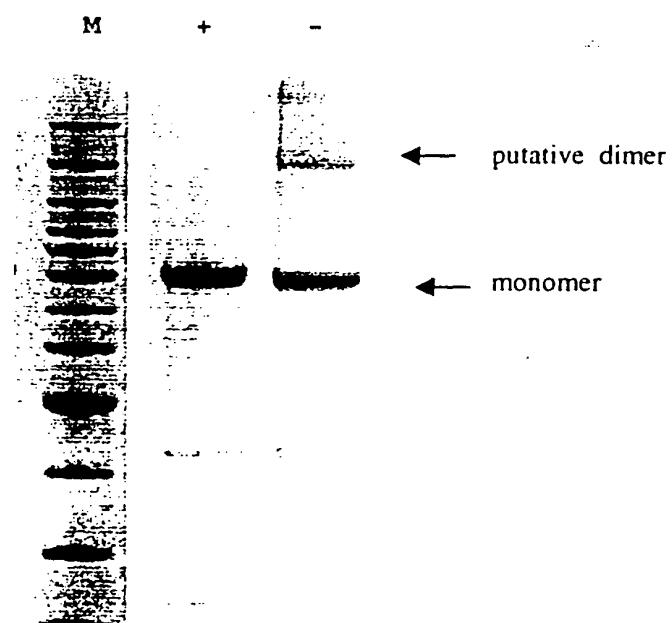
041869198

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FIG. 22. Disulphide-linked dimerisation of VEGF-X

(A) Mammalian cell expression



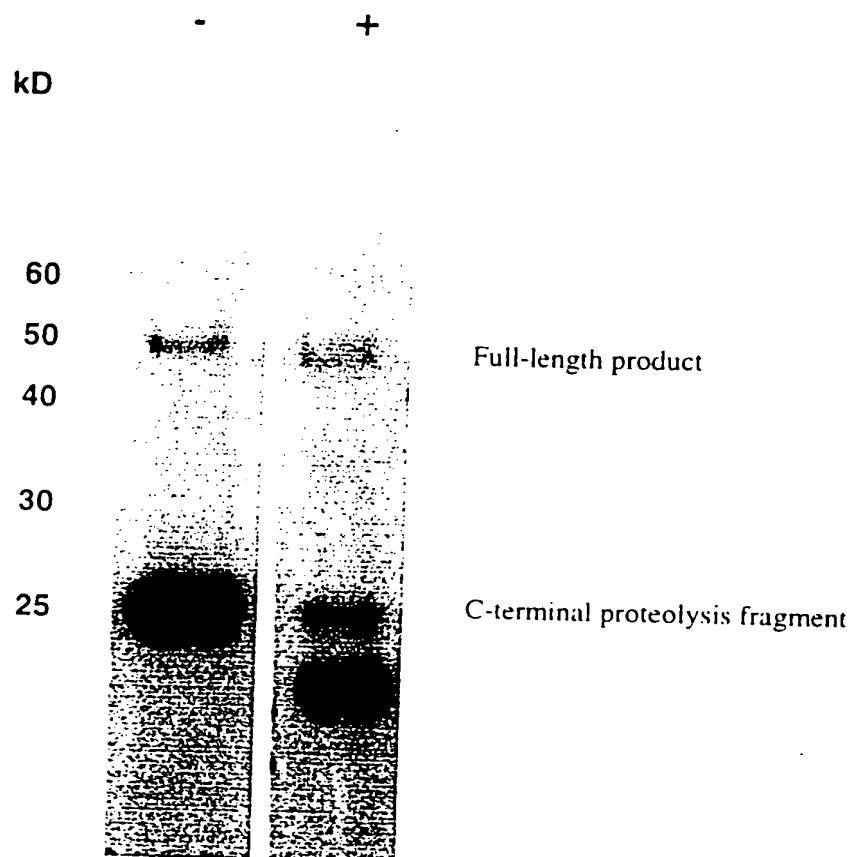
(B) *E.coli* expression



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FIG. 23. Glycosylation of VEGF-X



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FIG. 24.

DNA and polypeptide sequence used for *E.coli* expression of the PDGF-like domain

+3 M R G S H H H H H H H G M A S M
1 AAGGAGATAT ACATATGCGG GGTCTCATC ATCATCATCA TCATGGTATG GCTAGCATGA

+3 T G G O Q M G R D L Y D D D D K D P G R
61 CTGGTGGACA GCAAATGGGT CGGGATCTGT ACGACGATGA CGATAAGGAT CCGGGAAAGAA

+3 K S R V V D L N L L T E E V R L Y S C T
121 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC

+3 P R N F S V S I R E E L K R T D T I F W
181 CTCGTAACCTT CTCAGTGTCC ATAAGGAAG AACTAAAGAG ACCGATACC ATTTCTGGC

+3 P G C L L V K R C G G N C A C C L H N C
241 CAGGTTGTCT CCTGGTTAAA CGCTGTGCTG CGAACTGTGC CTGTTGTCTC CACAAATTGCA

+3 N E C Q C V P S K V T K K Y H E V L Q L
301 ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAATAATA CCACGAGGTC CTTCAGTTGA

+3 R P K T G V R G L H K S L T D V A L E H
361 GACCAAAGAC CGGTGTCAAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+3 H E E C D C V C R G S T G G
421 ATGAGGAGTG TCACTGTGTG TGCAGAGGGA GCACAGGAGG AATATGAATT CGAAGCTTGA

481 TCCGGCTGCT AACAAAGCCC

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FIG. 25. Expression of PDGF domain in *E.coli*



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FIG. 26.

DNA and polypeptide sequence used for *E.coli* expression of the CUB-like domain

+2 M A M D I G I N S D P E S H H H H H H H
1 GGCATGGCC ATGGATATCG GAATTAATTG GGATCCGGAG TCTCACCACATC ACCACCATCA

+2 E S N L S S K F Q F S S N K E Q N G V Q
61 TGAATCCAAC CTGAGTAGTA AATTCCAGTT TTCCAGCAAC AAGGAACAGA ACGGAGTACA

+2 D P Q H E R I I T V S T N G S I H S P R
121 AGATCCTCAG CATGAGAGAA TTATTACTGT GTCTACTAAT GGAAGTATTG ACAGCCCCAAG

+2 F P H T Y P R N T V L V W R L V A V E E
181 GTTCCTCAT ACTTATCCAA GAAATACGGT CTTGGTATGG AGATTAGTAG CAGTAGACCA

+2 N V W I Q L T F D E R F G L E D P E D D
241 AAATGTATGG ATACAACCTTA CGTTTGATGA AAGATTTGGG CTTGAAGACC CAGPAGATGA

+2 I C K Y D F V E V E E P S D G T I L G R
301 CATATGCAAG TATGATTTG TAGAAGTTGA GGAACCCAGT GATGGAACTA TATTAGGGCG

+2 W C G S G T V P G K Q I S K G N Q I R I
361 CTGGTGTGGT TCTGGTACTG TACCAAGAAA ACAGATTTCT AAAGGAAATC AAATTAGGAT

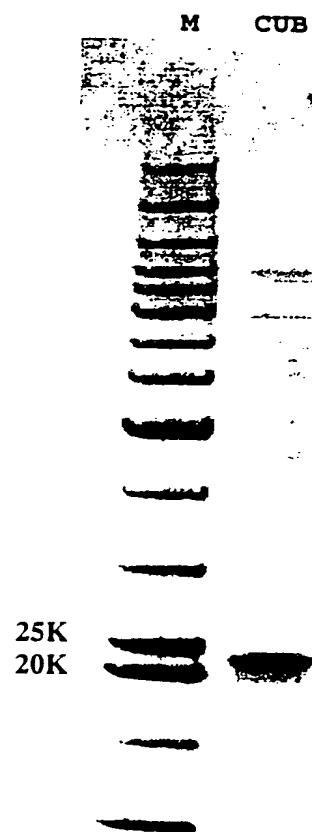
+2 R F V S D E Y F P S E P G F C I H Y N I
421 AAGATTTGTA TTGATGAAT ATTTCTTC TGAAACCAGGG TTCTGCATCC ACTACAACAT

+2 V M P Q F T E A V
481 TGTATGCCA CAATTACAG AAGCTGTGTA GTGAGCTCC GTGACAAAGC TTGGGGCCGC
541 ACTCGAGCAC

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FIG. 27. Expression of the CUB domain in *E.coli*

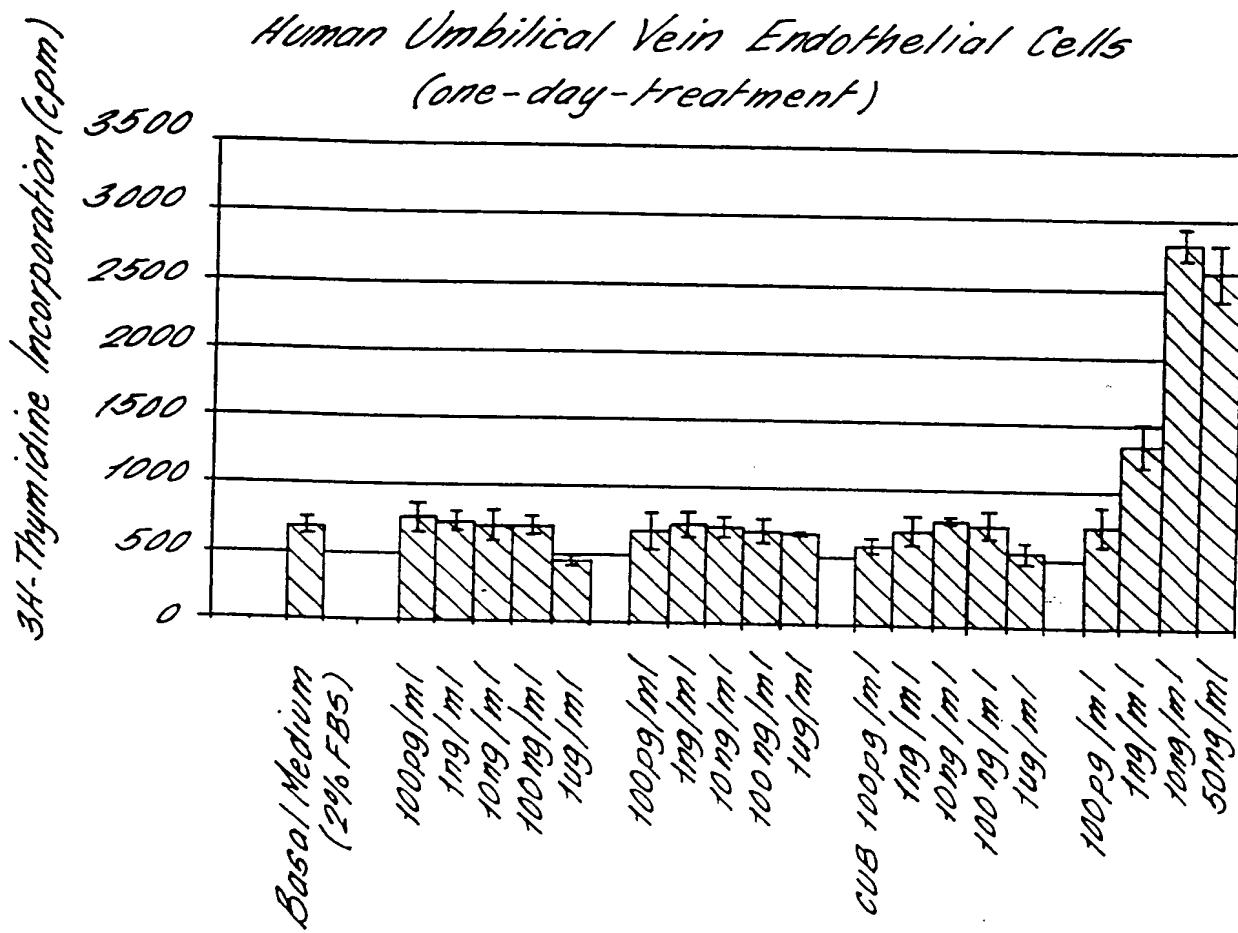


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FIG. 28. The Effect of Truncated VEGF-X
(CUB domain) on HUVEC Proliferation.

(A)



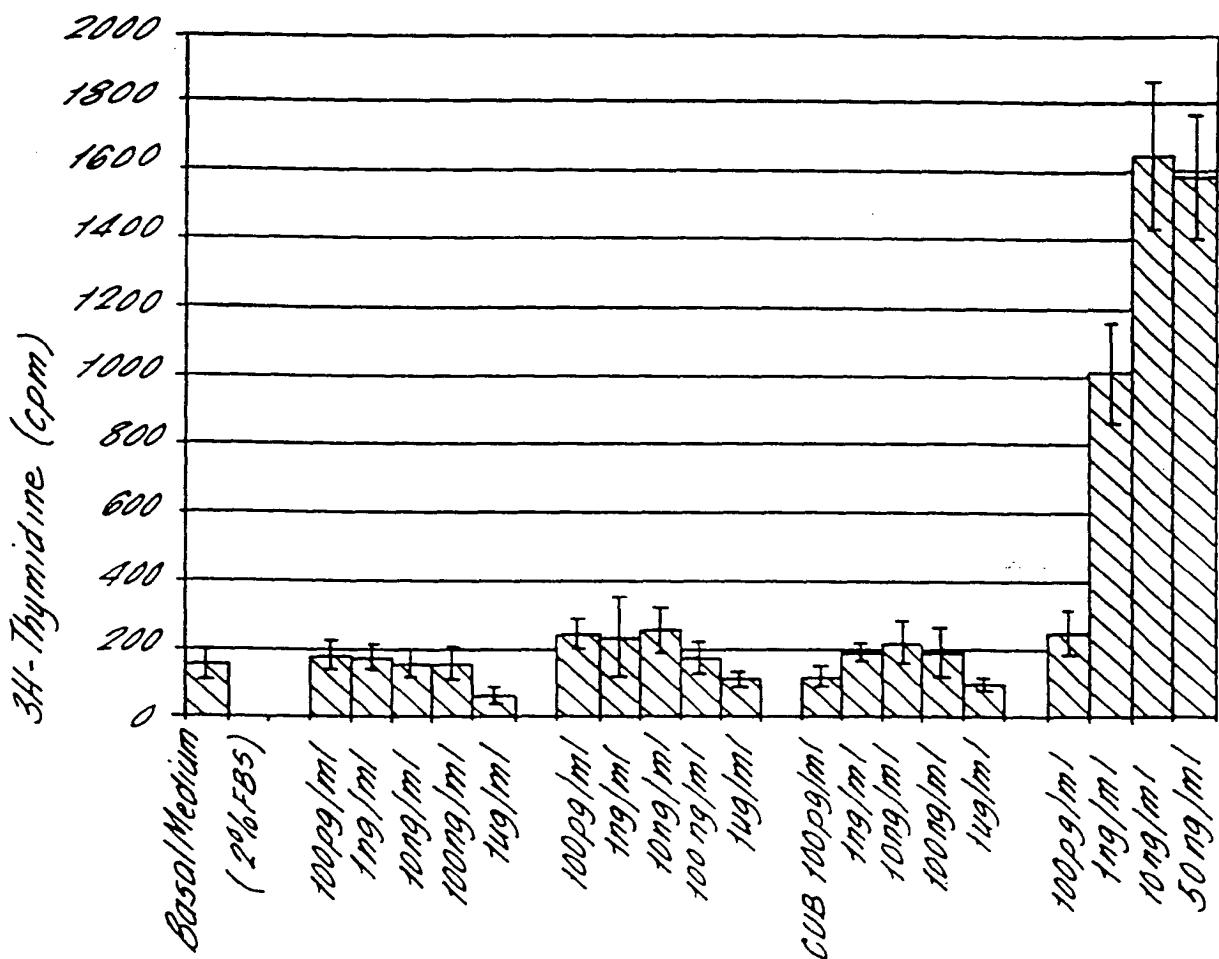
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FIG. 28 (CONTINUED 1).

(B)

Human Umbilical Vein Endothelial Cells (24-hour-starving Followed by one-day-treatment)

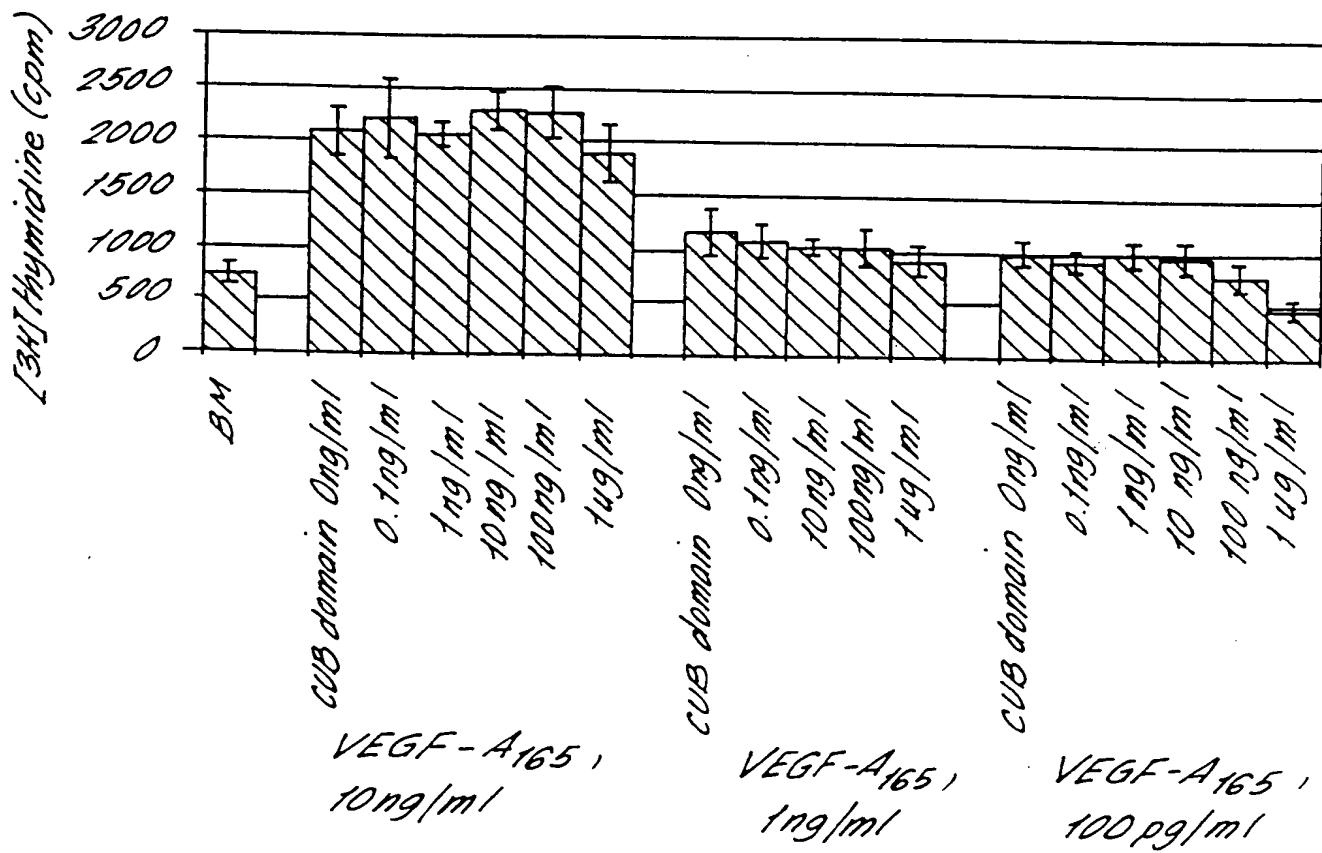


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FIG. 28 (CONTINUED 2).

(C)

The effect of VEGF-A₁₆₅ and VEGF-X CUB domain on the proliferation of HUVEC (two-day-treatment).



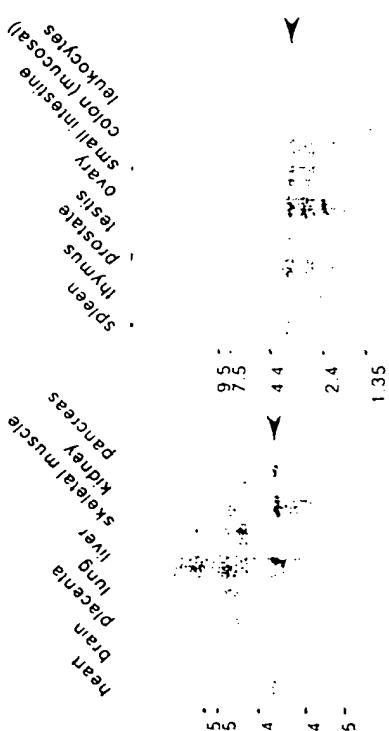
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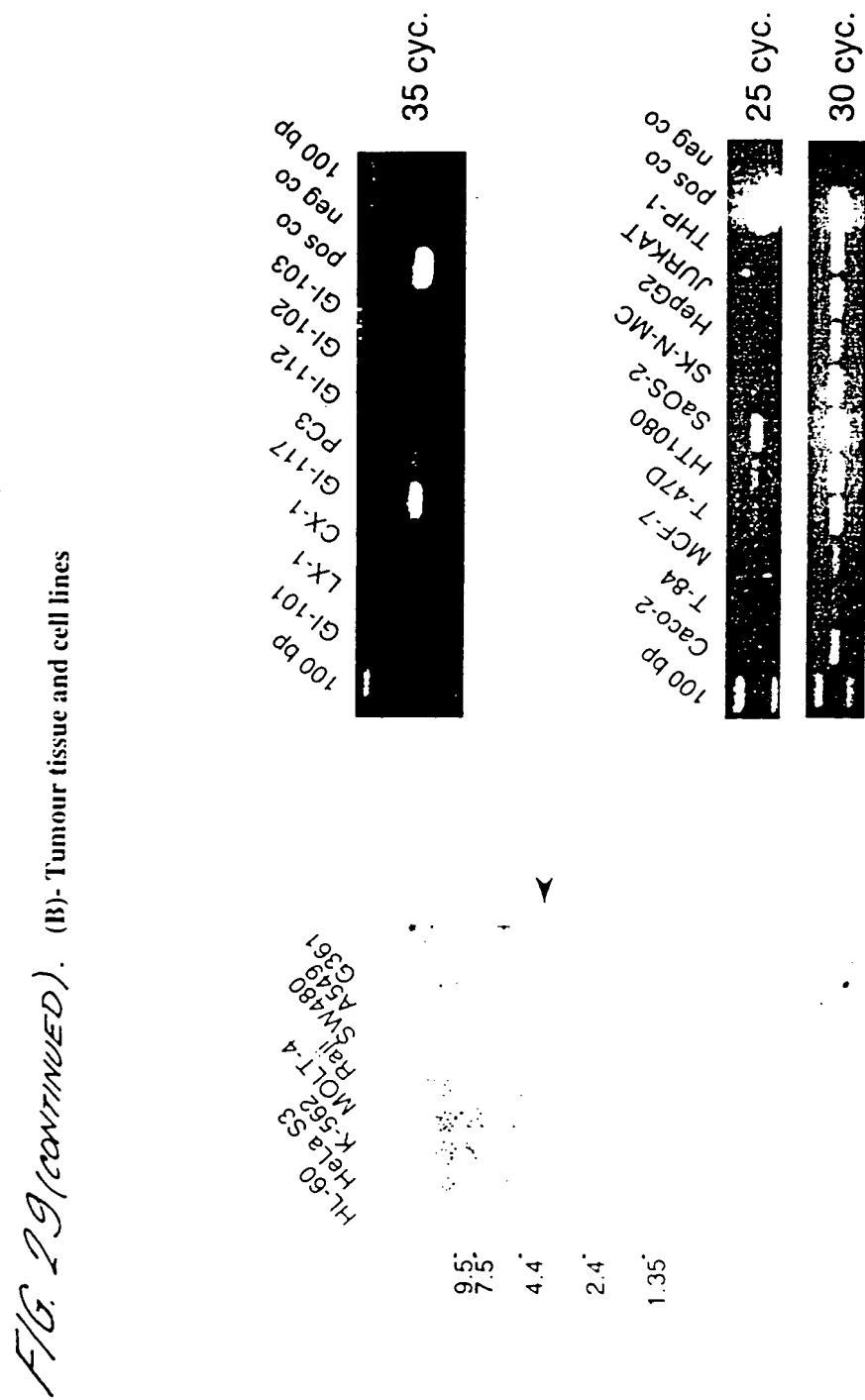
FIG. 29. Tissue distribution of mRNA

(A) - Normal tissues



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FIG. 30.

Partial intron/exon structure of the VEGF-X gene

(A) - Genomic DNA sequences of 2 exons determined by sequencing

tttccccatataccatatagtggatctgaaccagGGTCTGCATCCACTACAACATTGTCATGCCACAATTCAAGAGCTGTG
AGTCCTTCAGTGCTACCCCCCTTCAGCTTGCCACTGGACCTGCTTAATAATGCTATACTGCCTTAGTACCTTGGAAAGACCTTAT
TCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTGTT
TTGGAAAGAAAATCCAGAGTGGTGGATCTGAACCTCTAACAGAGGGAGGTAAAGATTATACAGCTGCACACCTCGTAACCTCTCAGT
TCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTCTGGCCAGGTTGTCTCTGGTAAACGCTGTGGTGGAACTGTGCCTG
TTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGgttaggtatacaatcccccc
ggcccccccggtatttatgttt

aaaggccagtcatagacattcggtgatttaaaagtggcttactttatcccttcagGTCCTTCAGTTGAGACCAAGACCCGT
GTCAGGGCATTGACAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTCAGAGGGAGCACAGGAGG
ATAGCCGCATACCACCAAGCAGCTTGCCCAGAGCTGTGAGTCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCAT
CCTTAATCTCAGTTGTTGTTCAAGGACCTTCATCTTCAGGATTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAG
GAGTTGTGCAACAGCTTTGAGAGGAGGCCAAAGGACAGGGAAAAGGTCTCAATCGTGGAAAGAAAATTAAATGTTGTATT
AAATAGATCACCAGCTAGTTCAGAGTTACCATGTACGTATTCACTAGCTGGGTCGTATTCAGTTCTTCGATAACGGCTTAG
GGTAATGTCAGTACAGGAAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCCTGGCTTAACCTAAAGCTCATGTCCTGGC
CTAAAATGTATAAAATCTGGATTTTTTTTTTGCGCATATTACATATGTAACCAAGAACATTCTATGTAACAAACC
TGGTTTTAAAAAGGAACATATGTCATGAAATTAAACTTGTGTCATGCTGATAGGACAGACTGGATTTCATATTCTTATTAA
AATTCTGCCATTAGAAGAGAACTACATTGTTGAGAGATAAAACCTGAAAGAGAAGAGTGGCCTTATCTTCACTTTA
TCGATAAGTCAGTTATTTGTTCATGTGTCACATTTCATATTCTCCCTTTGACATTATAACTGTTGGCTTTCTAATCTTGTAA
AATATATCTATTTCACCAAAGGTATTTAATATTCTTTATGACAACCTAGCATCAACTATTTAGCTGGTAATTTCCTAA
ACACAATTGTTATAGCCAGAGGAAACAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTCATTCTGATGGTG
CTAGAGTTAGATTAACTGCAATTAAAACACTGAATTGGAATAGAAATTGTAAGTGTGCAAAGACTTTGAAATAATTAAATTAA
TCATATCTCCATTCTGTTATGGAGATGAAATAAAAGCAACTTATGAAAGTAGACATTGACATCCAGCATTACTAACCTAT
TCCTTTTTGGGAAATCTGAGGCTAGCTCACAAAAACATAAGCACCTGAAAGACTTGGCAGCTTCCTGATAAAGCGTGTG
TGCTGTGCACTGAGAACACATCTATTATGTGATGTTGTCGTTTATTACTTAAACTCTGTTCCATACACTTGTATAAAATACA
TGGATATTTCATGTACAGAAGTATGTCCTAACAGATTCACTTATTGACTCTGGCAATTAAAAGAAAATCAGTAAATATT
TGCTTGAAATGCTTAATATGTCGCTAGGTTATGTCGTCAGTATTGAACTCAAAATGAAATGTCGTTTAAAGGAAATGAAATG
GGCTATTGGGGAGAAAATTatgtgtgtgtgtcaagatatttttgtggactctgagaaaatgaaagataaa

FIG. 30 (CONTINUED 1). 48/54

(B) - Location of splice sites within the cDNA sequence

1 GAATTGCCCTTTGTTAA ACCTTGGAA CTGGTCAGG TCCAGGTTT GCTTGATCC
 61 TTTCAAAAAA CTGGAGACAC AGAAGAGGGC TCTAGGAAA AGTTTGGAT GGGATTATGT
 121 GGAAACTACC CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG
 181 CCTTCCCCTG GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG
 +3 M S L F G L L L L T S
 241 AGTGAGCTCT CACCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG
 +3 A L A G Q R Q G T Q A E S N L S S K F Q
 301 CCCTGGCCGG CCAGAGACAG GGGACTCAGG CGGAATCCA CCTGAGTAGT AAATTCCAGT
 +3 F S S N K E Q N G V Q D P Q H S R I I T
 361 TTTCCAGCAA CAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG
 +3 V S T N G S I H S P R F P H T Y P R N T
 421 TGTCTACTAA TGGAAGTATT CACAGCCAA GGTTCTCA TACTTATCCA AGAAATACGG
 +3 V L V W R L V A V E E N V W I Q L T F D
 481 TCTTGGTATG GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACTACTT ACGTGGATG
 +3 E R F G L E D P E D D I C K Y D F V E V
 541 AAAGATTGG GCTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTT GTASAAGTTG
 +3 E E P S D G T I L G R W C G S G T V P G
 601 AGGAACCCAG TGATGAACT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA
 +3 K Q I S X G N Q I R I R F V S D E Y F P
 661 AACAGATTTC TAAGGAAAT CAAATTAGGA TAAGATTGT ATCTGATGAA TATTTCCCTT
 +3 S E P | G F C I H Y N I V M P Q F T E A V
 721 CTGAACCAAG GTCTGCATC CACTACAACA TTGTCAATGCC ACAATTACA GAAGCTGTGA
 +3 S P S V L P P S A L P L D L L N N A I T
 781 GTCCTTCAGT GCTACCCCT TCAGCTTGC CACTGGACCT GCTTAATAAT GCTATAACTG
 +3 A F S T L E D L I R Y L E P E R W Q L D
 841 CCTTTAGTAC CTGGAAAGAC CTTATTCGAT ATCTGAAAC AGAGAGATGG CAGTGGACT
 +3 L E D L Y R P T W Q L L G K A F V F G R
 901 TAGAGATCT ATATAGGCCA ACTTGGCAAC TTCTGGCAA GGCTTTGTT TTTGAAAGAA
 +3 K S R V V D L N L L T E E R L Y S C T
 961 AATCCAGAGT GGTGGATCTG AACCTTCAA CAGAGGAGT AAGATTATAAC AGCTGCACAC
 +3 P R N F S V S I R E E L K R T D T I F W
 1021 CTCGTAACTT CTCAGTGTCC ATAAGGGAAAG AACTAAAGAC AACCGATACC ATTTCTGGC
 +3 P G C L L V K R C G G N C A C C L H N C
 1081 CAGGGTCTCT CCTGGTTAAA CGCTGTGGTG CGAAGTGTGC CTGTTGTCTC CACAATTGCA
 +3 N E C O C V P S K V T K K Y H E | V L Q L

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FIG. 30 (CONTINUED 2).

+3 R P K T G V R G L H K S L T D V A L E H
 1201 GACCAAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+3 H E E C D C V C R G S T G G
 1261 ATGAGGAGTG TGACTGTGTG TGCGAGGGGA GCACAGGGAGG ATAGCCGCAT CACCACCCAGC

1321 AGCTCTTGCCTT CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCCTTAT

1381 CTCCATCCTT AATCTCAGTT GTTGCCTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC

1441 ATTCTGAAAG ACGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT TTTGAGAGGA

1501 GGCCTAAAGG ACACGGAGAA AGGTCTCAA TCGTGGAAAG AAAATTAAAT GTTGTATTAA

1561 ATAGATCACC AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTTCTGTAT

1621 TTCAGTTCTT TCGATACGGC TTAGGGTAAT GTCAAGTACAG GAAAAAAACT GTGCAAGTGA

1681 GCACCTGATT CGGTGCCTT GCTTAACCTCT AAAGCTCCAT GTCCTGGGCC TAAAATCGTA

1741 TAAAATCTGG ATTTTTTTT TTTTTTTTG CTCATATTCA CATATGTAAA CCAGAACATT

1801 CTATGTACTA CAAACCTGGT TTTTAAAGG GAACTATGTT GCTATGAATT AACTTGTGT

1861 CATGCTGATA CGACAGACTG GATTTTCAT ATTTCTTATT AAAATTCTG CCATTTAGAA

1921 GAAGAGAACT AGATTCATGG TTTGGAAAGAG ATAAACCTGA AAAGAAGAGT CCCCTTATCT

1981 TCACTTTATC GATAAGTCAG TTTATTGTT TCATTGTGT AATTTCATA TTCTCCTTT

2041 GACATTATAA CTGGTGGCTT TTCTAATCTT GTAAATATA TCTATTTTA CCAAAAGGTAT

2101 TTAATATTCT TTTTATGAC AACTTAGATC AACTATTTT AGCTTGGTAA ATTTTCTAA

2161 ACACAATTGT TATAGCCAGA CGAACAAAGA TGATATAAAA TATTGTTGCT CTGACAAAAAA

2221 TACATGTATT TCATTCCTGT ATGGTGCTAG AGTTAGATTA ATCTGCATTT TAAAAAAACTG

2281 AATTGGATA GATTTGGTAA GTTGCAAAGA CTTTTGAAA ATAATTAAAT TATCATATCT

2341 TCCATTCCCTG TTATTGGAGA TGAAAATAAA AAGCAACTTA TGAAAGTAGA CATTCAAGATC

2401 CAGCCATTAC TAACCTATTG CTTTTTGCG GAAATCTGAG CCTAGCTCAG AAAAACATAA

2461 AGCACCTTGA AAAAGACTTG CGACGCTTCCT GATAAAAGCGT GCTGTGCTGT GCAGTAGGAA

2521 CACATCCTAT TATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATAACACTTG

2581 TATAAAATACA TGGATATTTT TATGTACAGA AGTATGTCTC TTAACCAGTT CACTTATTGT

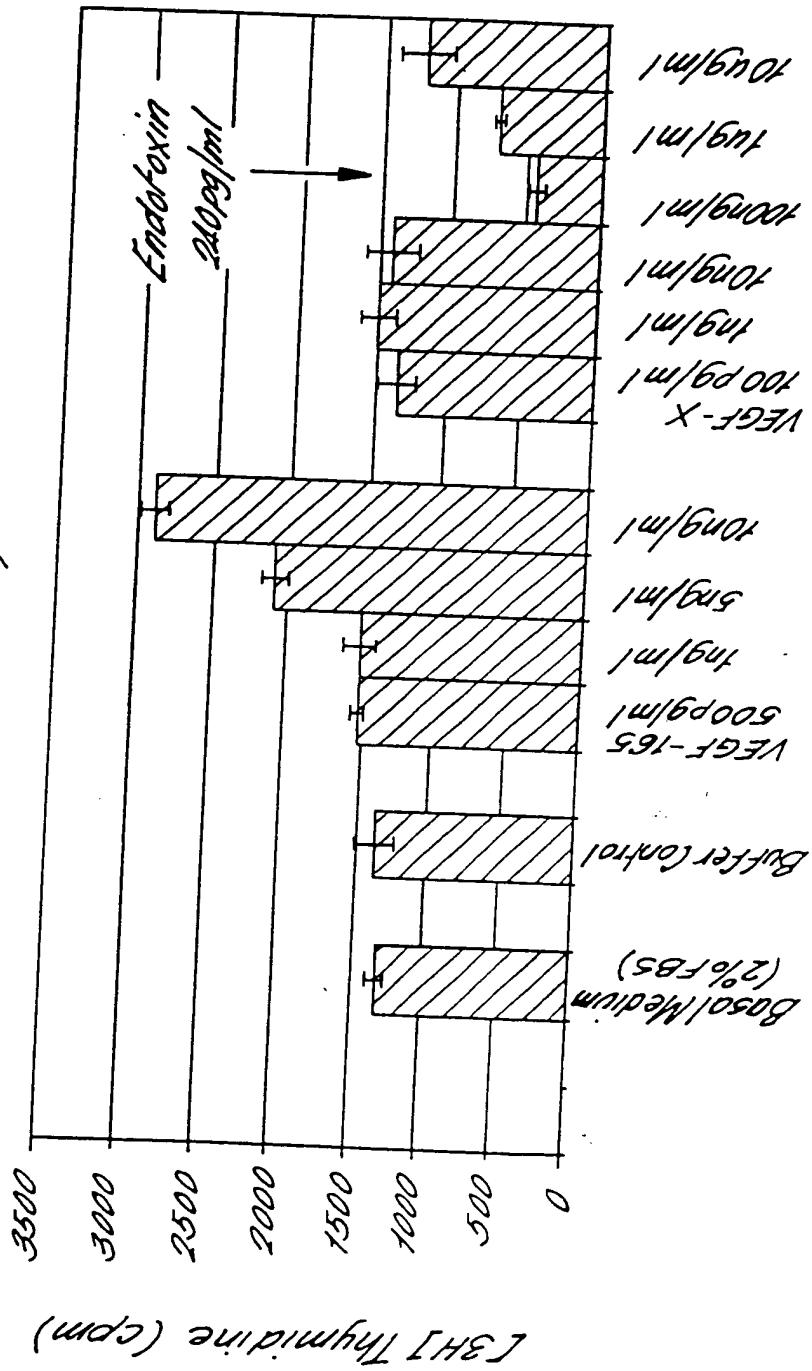
2641 ACCTGGAAAGG CGCAATTCTG CAGATATC

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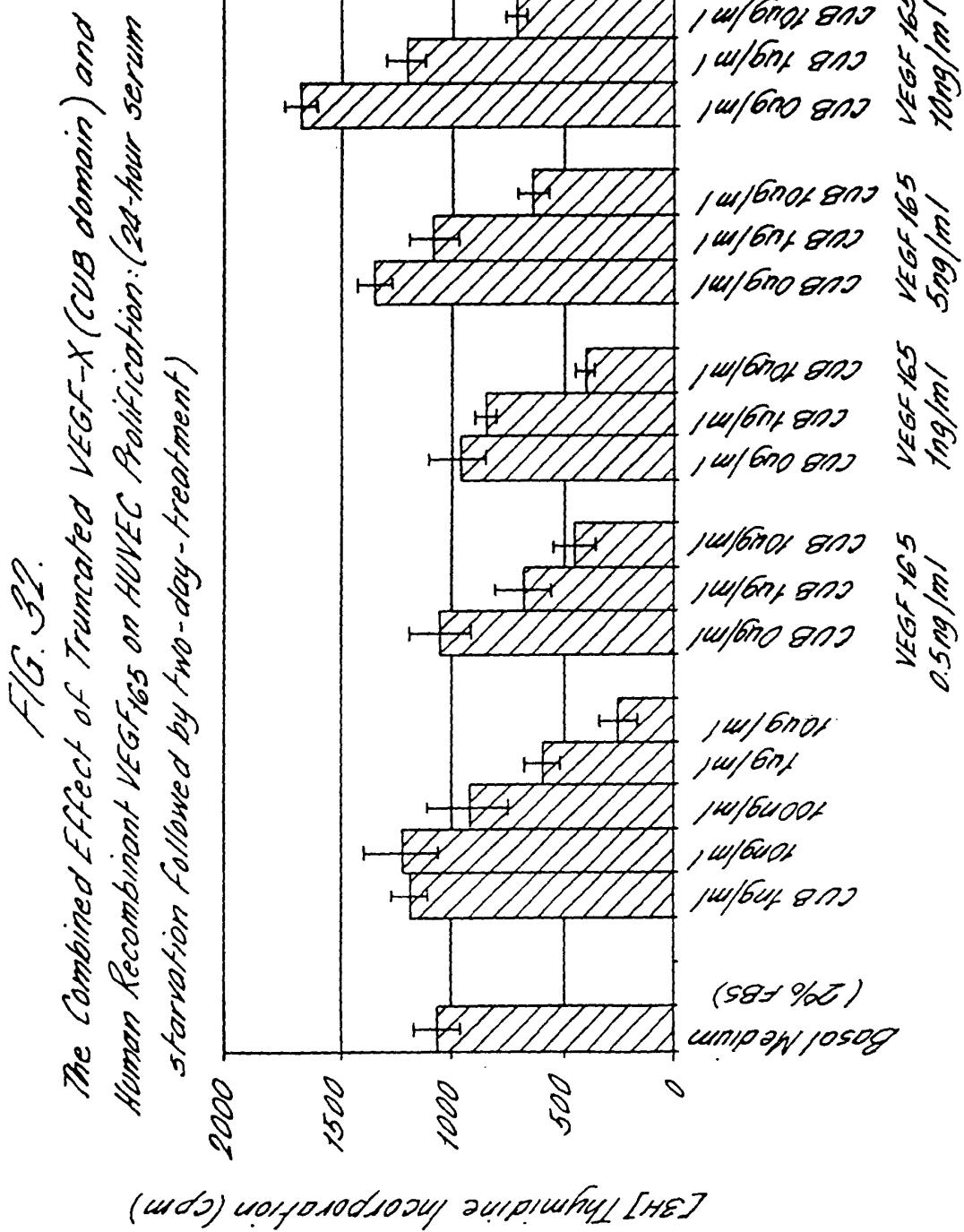
FIG. 31.

The Effect of F2-VEGF-X on HUVEC Proliferation:
(24-hour serum starvation followed by
one day-treatment)



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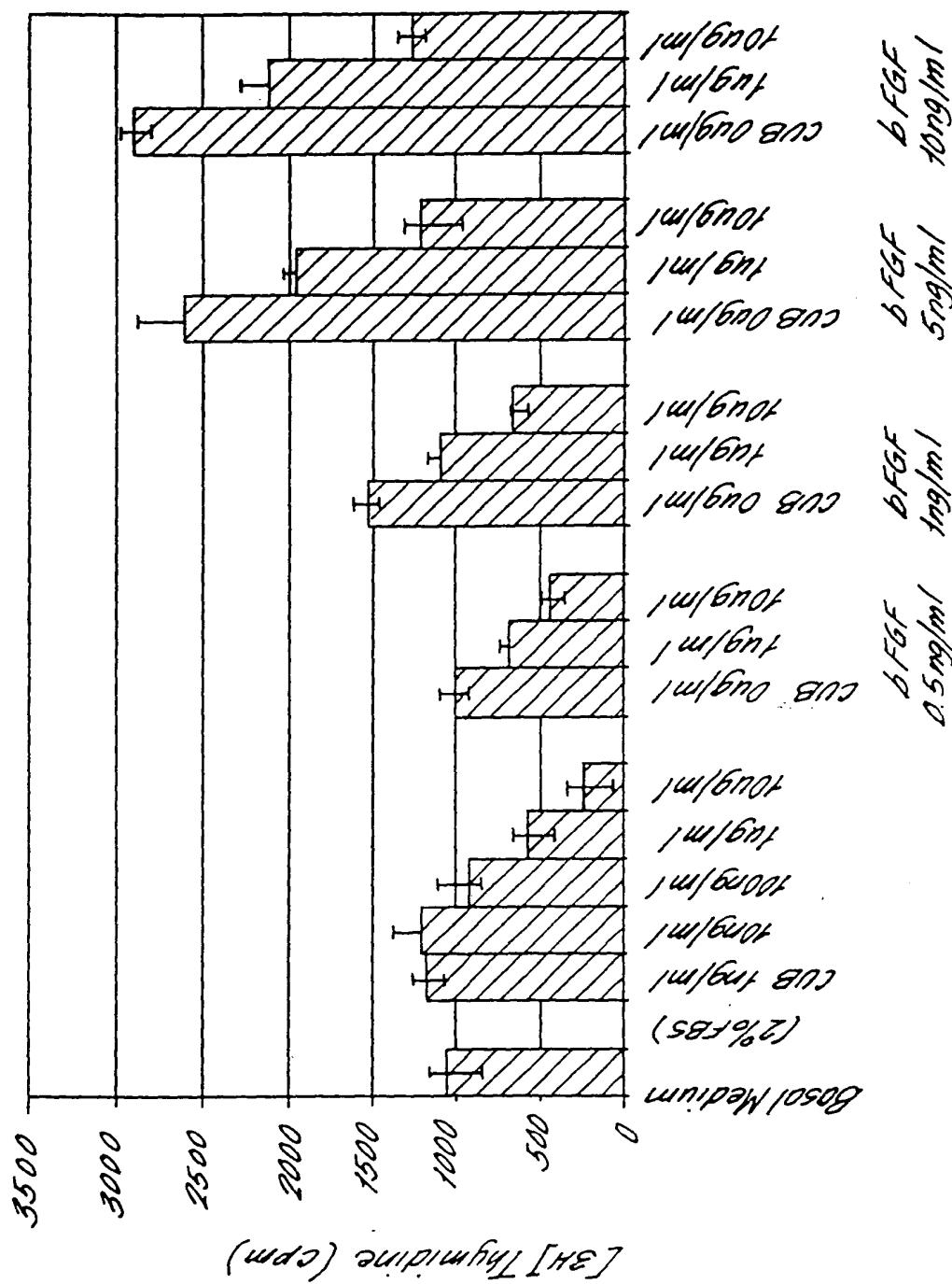
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Fig. 3.3.

The Combined Effect of CUB Domain and Human Recombinant bFGF on HUVEC Proliferation: (24-hour serum starvation followed by two-day-treatment).

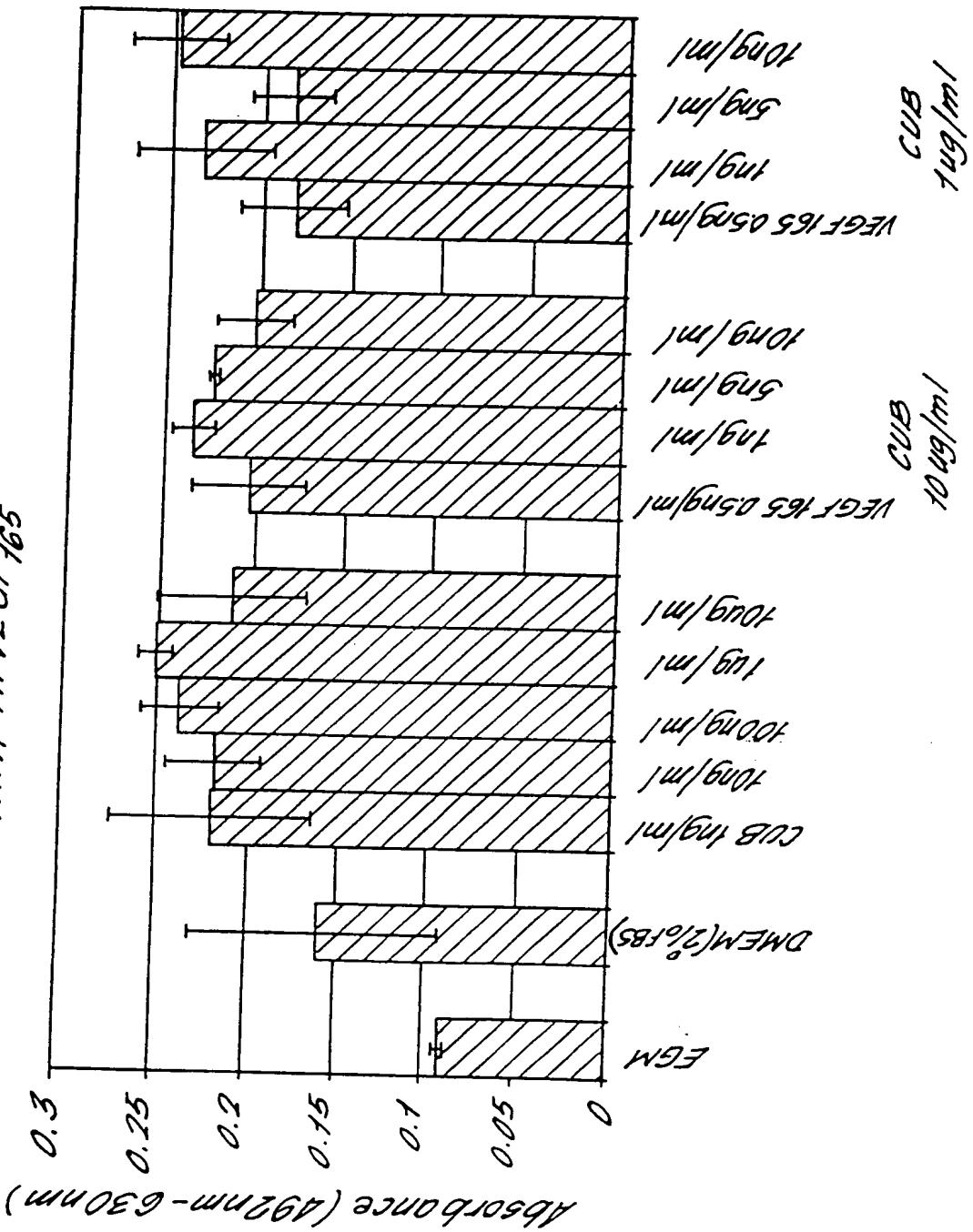


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FIG. 34.

LDH Assay For Testing Cytotoxicity of CUB Domain or
CUB Domain with rh VEGF165



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FIG. 3.5.

LDH Assay for Testing Cytotoxicity of cub Domain or
 cub Domain with rh- b FGF

